

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:40:57 ; Search time 11.4389 Seconds
(without alignments)
1690.542 Million cell updates/sec

Title: US-10-624-932-2_COPY_246_295

Perfect score: 290

Sequence: 1 STWTEWSVCSASCGRGWQKR.....NGGAFCEGQNVQKTACATLC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
1	290	100.0	330	8	ADH71620	Adh71620 Human pro
2	290	100.0	336	8	ADH71614	Adh71614 Human pro
3	290	100.0	898	2	AAW78898	Aaw78898 Rat UNC-5
4	290	100.0	898	5	AAU10543	Aau10543 Rat netri
5	290	100.0	898	5	AAU85403	Aau85403 Human pro
6	290	100.0	898	5	AAU97899	Aau97899 Human net
7	290	100.0	898	5	AAU97900	Aau97900 Rat netri
8	290	100.0	898	7	ADG42580	Adg42580 Rat trans
9	290	100.0	898	8	ADH71618	Adh71618 Human pro

10	290	100.0	943	4	AAM79128	Aam79128 Human pro
11	249	85.9	636	8	ADR99262	Adr99262 Splice va
12	249	85.9	669	8	ADR99252	Adr99252 Human sRO
13	249	85.9	929	7	ADG42583	Adg42583 Human tra
14	249	85.9	931	4	AAB50691	Aab50691 Human UNC
15	249	85.9	931	7	ADE63098	Ade63098 Human Pro
16	249	85.9	931	7	ADG42582	Adg42582 Mouse tra
17	249	85.9	931	7	ADG42584	Adg42584 Human tra
18	249	85.9	931	7	ABU64297	Abu64297 Human thr
19	249	85.9	931	8	ADR99258	Adr99258 Human unc
20	249	85.9	964	8	ADR99250	Adr99250 Human 1RO
21	249	85.9	982	4	ABG11551	Abg11551 Novel hum
22	243	83.8	331	8	ADH71612	Adh71612 Human pro
23	243	83.8	898	8	ADH71626	Adh71626 Human pro
24	243	83.8	899	5	AAU79939	Aau79939 Human UNC
25	243	83.8	899	7	ADG42569	Adg42569 Novel hum
26	243	83.8	899	8	ADH71636	Adh71636 Human pro
27	243	83.8	899	8	ADH71642	Adh71642 Human pro
28	243	83.8	899	8	ADH71648	Adh71648 Human pro
29	243	83.8	899	8	ADH71632	Adh71632 Human pro
30	243	83.8	899	8	ADH71610	Adh71610 Human pro
31	243	83.8	899	8	ADH71628	Adh71628 Human pro
32	243	83.8	899	8	ADH71640	Adh71640 Human pro
33	243	83.8	899	8	ADH71630	Adh71630 Human pro
34	243	83.8	899	8	ADH71650	Adh71650 Human pro
35	243	83.8	899	8	ADH71644	Adh71644 Human pro
36	243	83.8	899	8	ADH71634	Adh71634 Human pro
37	243	83.8	899	8	ADH71646	Adh71646 Human pro
38	243	83.8	899	8	ADH71638	Adh71638 Human pro
39	239	82.4	56	7	ADC77400	Adc77400 Human tra
40	239	82.4	321	8	ADQ65811	Adq65811 Novel hum
41	239	82.4	679	6	ABU52369	Abu52369 Human GPC
42	239	82.4	679	8	ADL24073	Adl24073 Human NOV
43	239	82.4	887	7	ADC77422	Adc77422 Human tra
44	239	82.4	924	6	ABU11210	Abu11210 Human G-p
45	239	82.4	933	5	AAO18734	Aao18734 Human NOV

ALIGNMENTS

RESULT 1

ADH71620

ID ADH71620 standard; protein; 330 AA.

XX

AC ADH71620;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21f SEQ ID NO:516.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.

XX

OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.

PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71619.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 516; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The

CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 330 AA;

Query Match 100.0%; Score 290; DB 8; Length 330;
Best Local Similarity 100.0%; Pred. No. 8.4e-25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 221 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 270

RESULT 2

ADH71614

ID ADH71614 standard; protein; 336 AA.

XX

AC ADH71614;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21c SEQ ID NO:510.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.

PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71613.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 510; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 336 AA;

Query Match 100.0%; Score 290; DB 8; Length 336;
Best Local Similarity 100.0%; Pred. No. 8.6e-25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 273

RESULT 3

AAW78898

ID AAW78898 standard; protein; 898 AA.

XX
AC AAW78898;
XX
DT 25-MAR-2003 (revised)
DT 21-DEC-1998 (first entry)
XX
DE Rat UNC-5 homologue UNC5H-1.
XX
KW UNC-5; UNC5H-1; rat; netrin receptor; cell migration; axon guidance; diagnosis; therapy.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Peptide 580. .594
FT /note= "peptide used to raise rabbit polyclonal antisera"
XX
PN WO9837085-A1.
XX
PD 27-AUG-1998.
XX
PF 19-FEB-1998; 98WO-US003143.
XX
PR 19-FEB-1997; 97US-00808982.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;
XX
DR WPI; 1998-495364/42.
DR N-PSDB; AAV52940.
XX
PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
PT the biopharmaceutical industry.
XX
PS Claim 1; Page 19-22; 32pp; English.
XX
CC UNC5H-1 and UNC5H-2 (see AAW78900) are rat homologues of *Caenorhabditis elegans* UNC-5 protein. Their amino acid sequences were deduced from isolated unc5h cDNA clones (see AAV52940 and AAV52942) isolated from an E18 brain cDNA library. The predicted proteins show similarity with UNC-5, possess 2 predicted Ig-like domains and 2 predicted thrombospondin type-1 repeats, a predicted membrane spanning region, and a large intracellular domain. They are predicted to be involved in cell migration and axon guidance, and are characterised as receptor proteins for netrins. Human UNC5H-1 (see AAW78899) and UNC5H-2 (see AAW78901) proteins are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly from transfected host cells. The invention also provides unc-5 hybridisation probes and primers, vertebrate UNC-5-specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis (e.g. genetic hybridisation screens for vertebrate unc-5 transcripts), therapy (e.g. gene therapy to modulate vertebrate unc-5 gene expression) and in the biopharmaceutical industry (e.g. as immunogens, reagents for modulating cell guidance, reagents for screening chemical libraries for lead pharmacological agents, etc.).
CC (Updated on 25-MAR-2003 to correct PI field.)
XX

SQ Sequence 898 AA;
\\
Query Match 100.0%; Score 290; DB 2; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.3e-24;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 246 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 295

RESULT 4
AAU10543
ID AAU10543 standard; protein; 898 AA.
XX
AC AAU10543;
XX
DT 14-FEB-2002 (first entry)
XX
DE Rat netrin receptor UNC5H1 (YSG7) polypeptide.
XX
KW YSG; YSG7; schizophrenia; chronic animal model; LCGU; netrin receptor;
KW local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;
KW calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A;
KW epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic;
KW tumour necrosis factor alpha; TNF-alpha; rat.
XX
OS Rattus sp.
XX
PN WO200175440-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-GB001486.
XX
PR 31-MAR-2000; 2000GB-00007880.
PR 26-MAY-2000; 2000GB-00012768.
XX
PA (WELF-) WELFIDE CORP.
XX
PI Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;
XX
DR WPI; 2002-010813/01.
DR N-PSDB; AAS16843.
XX
PT Novel chronic animal model of schizophrenia, useful for identifying anti-
PT psychotic drugs and genes that are associated with schizophrenia.
XX
PS Disclosure; Fig 8b; 79pp; English.
XX
CC The invention relates to YSG polynucleotide fragments for use in
CC diagnosing and/or developing treatments for schizophrenia using chronic
CC animal models. The polynucleotides and their encoded polypeptides are
CC used for identification of compounds which modulate the expression of YSG
CC molecules, leading to the manufacture of schizophrenia medicaments. The
CC sequences can also be used for testing candidate compounds for any effect
CC on the polypeptides. Anti-schizophrenic effects of a compound can be

CC determined by measuring local cerebral glucose utilisation (LCGU) or
CC comparing its expression level with that of a control group. The
CC sequences are useful in the identification of genes associated with
CC schizophrenic states and in the development of an antibody. The sequences
CC of the invention include phosphodiesterase 1-alpha, calcium-independent
CC alpha-latrotoxin receptors (CIRL)-1,2&3, epithelial discoidin domain
CC receptor 1 (trkE), netrin receptor (UNC5H1), synapsins 1A and AB and
CC tumour necrosis factor (TNF) alpha. This sequence represents rat netrin
CC receptor UNC5H1 (YSG7) polypeptide

XX

SQ Sequence 898 AA;

Query Match 100.0%; Score 290; DB 5; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.3e-24;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50

||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 246 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 295

RESULT 5

AAU85403

ID AAU85403 standard; protein; 898 AA.

XX

AC AAU85403;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human protein NOV1.

XX

KW Human; NOVX; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200210216-A2.

XX

PD 07-FEB-2002.

XX

PF 30-JUL-2001; 2001WO-US024225.

XX

PR 28-JUL-2000; 2000US-0221409P.

PR 04-AUG-2000; 2000US-0222840P.

PR 04-AUG-2000; 2000US-0223752P.

PR 04-AUG-2000; 2000US-0223762P.

PR 04-AUG-2000; 2000US-0223769P.

PR 04-AUG-2000; 2000US-0223770P.

PR 14-AUG-2000; 2000US-0225146P.

PR 15-AUG-2000; 2000US-0225392P.
PR 15-AUG-2000; 2000US-0225470P.
PR 16-AUG-2000; 2000US-0225697P.
PR 01-FEB-2001; 2001US-0263662P.
PR 05-APR-2001; 2001US-0281645P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX
DR WPI; 2002-180074/23.
DR N-PSDB; ABK37922.
XX
PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX
PS Claim 1; Page 11; 213pp; English.
XX
CC The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence represents a
CC NOVX protein.

Query Match 100.0%; Score 290; DB 5; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.3e-24;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 STWTEWSVCSASCCRGWOKRSRSCTNRAPILNCCAECECONVOKTAGATLG 50

Qy 1 SWIIEWSVCSASCGRGWQRKRSCLNFAPLNGGAFCEGQNVRQIACATLQ

246. СТАНДАРТЫ ВОСПРОИМЧИВОСТИ ПОДСИСТЕМЫ СВЯЗИ С ПОДСИСТЕМЫ СВЯЗИ 245

AAU97899

ID AAU97899 standard; protein; 898 AA.

XX

AC AAU97899;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human netrin binding membrane receptor UNC5H-1 protein.

XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; human; nootropic; neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer; central nervous system; CNS; stroke; Parkinson's disease; multiple sclerosis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 152. .223

FT /note= "Immunoglobulin domain "

FT Domain 247. .294

FT /note= "Thrombospondine type 1 domain "

FT Domain 302. .348

FT /note= "Thrombospondine type 1 domain"

FT Region 361. .382

FT /note= "Transmembrane region"

FT Domain 495. .598

FT /note= "ZU5 domain"

FT Domain 817. .897

FT /note= "Death domain"

XX

PN WO200233080-A2.

XX

PD 25-APR-2002.

XX

PF 15-OCT-2001; 2001WO-EP011891.

XX

PR 16-OCT-2000; 2000US-0240061P.

XX

PA (FARB) BAYER AG.

XX

PI Koehler RH;

XX

DR WPI; 2002-463314/49.

DR N-PSDB; ABK52891.

XX

PT Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.

XX

PS Claim 1; Fig 2; 94pp; English.

XX

CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the

CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g., Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents the human netrin binding
CC membrane receptor UNC5H-1 protein of the invention

XX

SQ Sequence 898 AA;

Query Match 100.0%; Score 290; DB 5; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.3e-24;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 246 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 295

RESULT 7
AAU97900

ID AAU97900 standard; protein; 898 AA.

XX

AC AAU97900;

XX

DT 27-AUG-2002 (first entry)

XX

DE Rat netrin binding membrane receptor UNC5H-1 protein.

XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; Rat; nootropic;
KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;
KW central nervous system; CNS; stroke; Parkinson's disease;
KW multiple sclerosis; Alzheimer's disease.

XX

OS Rattus sp.

XX

FT	Key	Location/Qualifiers
FT	Domain	152. .223 /note= "Immunoglobulin domain "
FT	Domain	247. .294 /note= "Thrombospondine type 1 domain "
FT	Domain	302. .348 /note= "Thrombospondine type 1 domain"
FT	Region	361. .382 /note= "Transmembrane region"
FT	Domain	495. .598 /note= "ZU5 domain"
FT	Domain	817. .897 /note= "Death domain"

XX

PN WO200233080-A2.

XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-EP011891.
XX
PR 16-OCT-2000; 2000US-0240061P.
XX
PA (FARB) BAYER AG.
XX
PI Koehler RH;
XX
DR WPI; 2002-463314/49.
XX
PT Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.
XX
PS Disclosure; Fig 3; 94pp; English.
XX
CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g., Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents the Rat netrin binding
CC membrane receptor UNC5H-1 protein of the invention
XX
SQ Sequence 898 AA;

Query Match 100.0%; Score 290; DB 5; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.3e-24;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
|||
Db 246 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 295

RESULT 8
ADG42580
ID ADG42580 standard; protein; 898 AA.
XX
AC ADG42580;
XX
DT 26-FEB-2004 (first.entry)

XX
DE Rat transmembrane receptor Unc5H1.
XX
KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
KW NOVX-associated disorder; cancer; rat; transmembrane receptor; Unc5H1.
XX
OS Rattus norvegicus.
XX
PN US2003204052-A1.
XX
PD 30-OCT-2003.
XX
PF 04-OCT-2001; 2001US-00970944.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX
PA (HERR/) HERRMANN J L.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
XX
PI Herrmann JL, Rastelli L, Shimkets RA;
XX
DR WPI; 2003-900673/82.
XX
PT New NOVX gene or NOVX-specific antibody, useful for preparing a
PT composition for treating or preventing a NOVX-associated disorder, e.g.,
PT cancer.
XX
PS Disclosure; SEQ ID NO 13; 118pp; English.
XX
CC The invention describes a new isolated polypeptide comprising: a
CC polypeptide or its mature form comprising a sequence not given in the
CC specification; or a variant of (A), where one or more amino acid residues
CC in the variant differs in no more than 15% from the amino acid sequence
CC of the mature form. The pharmaceutical composition may be administered
CC via oral, transdermal, rectal or parenteral route. The polypeptide,
CC nucleic acid or antibody is useful for preparing a composition for
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
CC the amino acid sequence of a transmembrane receptor Unc5H1 used in a
CC comparison with the novel human proteins of the invention.
XX
SQ Sequence 898 AA;

Query Match 100.0%; Score 290; DB 7; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.3e-24;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 246 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 295

RESULT 9
ADH71618
ID ADH71618 standard; protein; 898 AA.
XX
AC ADH71618;

XX
DT 25-MAR-2004 (first entry)
XX
DE Human protein of the invention NOV21e SEQ ID NO:514.
XX
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71617.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK52261.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 20; Page 4148-4150; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 943 AA;

RESULT 11
ADR99262
ID ADR99262 standard; protein; 636 AA.
XX
AC ADR99262;
XX
DT 16-DEC-2004 (first entry)
XX
DE Splice variant human uncoordinated 5C (sUNC5C) protein.
XX
KW RAR-like orphan receptor alpha 1-uncoordinated 5C; ROR-alpha-1-UNC5C;
KW ROR-alpha-5; obesity; susceptibility; anorectic; antilipidaemic;
KW antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiant;

KW vasotropic; osteopathic; antiarthritic; cytostatic; gene therapy;
KW hyperlipidaemia; human; SUNC5C.
XX
OS Homo sapiens.
XX
PN WO2004083371-A2.
XX
PD 30-SEP-2004.
XX
PF 16-MAR-2004; 2004WO-GB001124.
XX
PR 19-MAR-2003; 2003GB-00006185.
XX
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
XX
PI Dahl N;
XX
DR WPI; 2004-691032/67.
DR N-PSDB; ADR99261.
XX
PT New isolated nucleic acid molecule encoding a RAR-like orphan receptor
PT alpha 1-uncoordinated 5C (RORapproximatelyal-UNC5C) polypeptide, useful
PT in diagnosing or treating obesity and hyperlipidemia.
XX
PS Disclosure; SEQ ID NO 14; 96pp; English.
XX
CC The invention relates to a novel isolated nucleic acid molecule,
CC comprising a nucleotide sequence having at least 65% identity to a
CC degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
CC (ADR99249, ADR99251 or ADR99255), or the complement of nucleotide
CC sequence with ADR99249, ADR99251 or ADR99255. The invention further
CC comprises: an isolated nucleic acid molecule encoding a RAR-like orphan
CC receptor alpha 1-uncoordinated 5C (ROR-alpha-1-UNC5C) polypeptide; an
CC isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
CC vector comprising any of the nucleic acid molecules as cited; a host cell
CC comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
CC UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
CC a method for producing a protein comprising culturing the host cell; a
CC method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
CC protein; a method for detecting the presence of an obesity susceptibility
CC gene; a method for detecting the presence of a translocation junction
CC between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
CC 15q22.2; a method for identifying a test compound that modulates the
CC expression of an obesity susceptibility gene identified in said method; a
CC method for identifying a test compound that modulates the activity of an
CC obesity protein encoded by the obesity susceptibility gene identified in
CC said method; a method for treating a subject having obesity; a
CC pharmaceutical composition comprising a compound identified in the
CC previous methods, and an adjuvant, diluent or carrier; making a
CC pharmaceutical composition; a method for determining if an obesity
CC susceptibility gene identified in the appropriate method; and a method
CC for diagnosing obesity, or a susceptibility to it in a subject. The
CC isolated nucleic acid molecules and compounds of the invention have the
CC following activities: anorectic, antilipaemic, antiarteriosclerotic,
CC hepatotropic, hypotensive, antidiabetic, cardiant, vasotropic,
CC osteopathic, antiarthritic, and cytostatic. The isolated nucleic acid

CC molecules and compounds may be used in gene therapy. The compound
CC modulating the activity of an obesity protein or the expression of an
CC obesity susceptibility gene is useful in the preparation of a medicament
CC for the treatment of obesity. The compound is also useful in treating or
CC diagnosing hyperlipidaemia, and the consequences of obesity, such as
CC arteriosclerosis, fatty liver, hypertension, diabetes, coronary heart
CC disease, stroke, gallbladder disease, osteoarthritis and cancer. This
CC sequence represents the alternative splice version of the human
CC uncoordinated 5C (UNC5C) protein of the invention.

XX

SQ Sequence 636 AA;

Query Match 85.9%; Score 249; DB 8; Length 636;
Best Local Similarity 82.0%; Pred. No. 7.5e-20;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50

|||||||:: ||||:||:||:||:|||||||||||||:||| || |||

Db 264 STWTEWSVCNSRCGRGYQKRRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

RESULT 12

ADR99252

ID ADR99252 standard; protein; 669 AA.

XX

AC ADR99252;

XX

DT 16-DEC-2004 (first entry)

XX

DE Human sROR-alpha-1-UNC5C protein.

XX

KW RAR-like orphan receptor alpha 1-uncoordinated 5C; ROR-alpha-1-UNC5C;
KW ROR-alpha-5; obesity; susceptibility; anorectic; antilipaemic;
KW antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiant;
KW vasotropic; osteopathic; antiarthritic; cytostatic; gene therapy;
KW hyperlipidaemia; human; sROR-alpha-1-UNC5C.

XX

OS Homo sapiens.

XX

PN WO2004083371-A2.

XX

PD 30-SEP-2004.

XX

PF 16-MAR-2004; 2004WO-GB001124.

XX

PR 19-MAR-2003; 2003GB-00006185.

XX

PA (ASTR) ASTRAZENECA AB.

PA (ASTR) ASTRAZENECA UK LTD.

XX

PI Dahl N;

XX

DR WPI; 2004-691032/67.

DR N-PSDB; ADR99251.

XX

PT New isolated nucleic acid molecule encoding a RAR-like orphan receptor
PT alpha 1-uncoordinated 5C (RORapproximately1-UNC5C) polypeptide, useful

PT in diagnosing or treating obesity and hyperlipidemia.

XX

PS Claim 9; SEQ ID NO 4; 96pp; English.

XX

CC The invention relates to a novel isolated nucleic acid molecule,
CC comprising a nucleotide sequence having at least 65% identity to a
CC degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
CC (ADR99249, ADR99251 or ADR99255), or the complement of nucleotide
CC sequence with ADR99249, ADR99251 or ADR99255. The invention further
CC comprises: an isolated nucleic acid molecule encoding a RAR-like orphan
CC receptor alpha 1-uncoordinated 5C (ROR-alpha-1-UNC5C) polypeptide; an
CC isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
CC vector comprising any of the nucleic acid molecules as cited; a host cell
CC comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
CC UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
CC a method for producing a protein comprising culturing the host cell; a
CC method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
CC protein; a method for detecting the presence of an obesity susceptibility
CC gene; a method for detecting the presence of a translocation junction
CC between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
CC 15q22.2; a method for identifying a test compound that modulates the
CC expression of an obesity susceptibility gene identified in said method; a
CC method for identifying a test compound that modulates the activity of an
CC obesity protein encoded by the obesity susceptibility gene identified in
CC said method; a method for treating a subject having obesity; a
CC pharmaceutical composition comprising a compound identified in the
CC previous methods, and an adjuvant, diluent or carrier; making a
CC pharmaceutical composition; a method for determining if an obesity
CC susceptibility gene identified in the appropriate method; and a method
CC for diagnosing obesity, or a susceptibility to it in a subject. The
CC isolated nucleic acid molecules and compounds of the invention have the
CC following activities: anorectic, antilipaemic, antiarteriosclerotic,
CC hepatotropic, hypotensive, antidiabetic, cardiant, vasotropic,
CC osteopathic, antiarthritic, and cytostatic. The isolated nucleic acid
CC molecules and compounds may be used in gene therapy. The compound
CC modulating the activity of an obesity protein or the expression of an
CC obesity susceptibility gene is useful in the preparation of a medicament
CC for the treatment of obesity. The compound is also useful in treating or
CC diagnosing hyperlipidaemia, and the consequences of obesity, such as
CC arteriosclerosis, fatty liver, hypertension, diabetes, coronary heart
CC disease, stroke, gallbladder disease, osteoarthritis and cancer. This
CC sequence represents the human sROR-alpha-1-UNC5C protein of the
CC invention.

XX

SQ Sequence 669 AA;

Query Match 85.9%; Score 249; DB 8; Length 669;
Best Local Similarity 82.0%; Pred. No. 7.9e-20;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||: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RESULT 13
ADG42583

ID ADG42583 standard; protein; 929 AA.
XX
AC ADG42583;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human transmembrane receptor Unc5 homologue #1.
XX
KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
KW NOVX-associated disorder; cancer; human; transmembrane receptor;
KW Unc5 homologue.
XX
OS Homo sapiens.
XX
PN US2003204052-A1.
XX
PD 30-OCT-2003.
XX
PF 04-OCT-2001; 2001US-00970944.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX
PA (HERR/) HERRMANN J L.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
XX
PI Herrmann JL, Rastelli L, Shimkets RA;
XX
DR WPI; 2003-900673/82.
XX
PT New NOVX gene or NOVX-specific antibody, useful for preparing a
PT composition for treating or preventing a NOVX-associated disorder, e.g.,
PT cancer.
XX
PS Disclosure; SEQ ID NO 16; 118pp; English.
XX
CC The invention describes a new isolated polypeptide comprising: a
CC polypeptide or its mature form comprising a sequence not given in the
CC specification; or a variant of (A), where one or more amino acid residues
CC in the variant differs in no more than 15% from the amino acid sequence
CC of the mature form. The pharmaceutical composition may be administered
CC via oral, transdermal, rectal or parenteral route. The polypeptide,
CC nucleic acid or antibody is useful for preparing a composition for
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
CC the amino acid sequence of a transmembrane receptor homologue used in a
CC comparison with the novel human proteins of the invention.
XX
SQ Sequence 929 AA;

Query Match 85.9%; Score 249; DB 7; Length 929;
Best Local Similarity 82.0%; Pred. No. 1.1e-19;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
|||:||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 264 STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

RESULT 14
AAB50691
ID AAB50691 standard; protein; 931 AA.
XX
AC AAB50691;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human UNC5C protein SEQ ID NO:90.
XX
KW Human; *Caenorhabditis elegans*; UNC-5; splice variant; nematode worm;
KW protein-protein interaction; identification.
XX
OS Homo sapiens.
XX
PN WO200073328-A2.
XX
PD 07-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-EP005108.
XX
PR 01-JUN-1999; 99GB-00012755.
XX
PA (DEVG-) DEVGEM NV.
XX
PI Van Crielinge W, Roelens I, Bogaert T, Verwaerde P;
XX
DR WPI; 2001-016508/02.
XX
PT Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a
PT human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
PT identifying unknown human cDNAs which encode proteins that interact with
PT the human unc-5C protein.
XX
PS Disclosure; Page 224-227; 246pp; English.
XX
CC The present invention describes 3 variants of human unc-5C cDNAs (unc-
CC 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-
CC 5C transcripts, and a human unc-5HS1 cDNA which shares homology with the
CC Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on
CC protein-protein-interactions between the unc-5 protein and a variety of
CC different interacting proteins. The unc-5C variant cDNAs and unc-5HS1
CC cDNA are useful in methods for identifying compounds which reduce or
CC inhibit the lethal phenotype associated with the expression of the unc-5
CC death domain in yeast. They are also useful in yeast two hybrid
CC experiments for identifying unknown human cDNAs which encode proteins
CC that interact with the human unc-5C protein. AAC90914 to AAC90971 and
CC AAB50646 to AAB50693 represent sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 931 AA;

Query Match 85.9%; Score 249; DB 4; Length 931;
Best Local Similarity 82.0%; Pred. No. 1.1e-19;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 264 STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

RESULT 15

ADE63098

ID ADE63098 standard; protein; 931 AA.

XX

AC ADE63098;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein AAC67491, SEQ ID NO 9033.

XX

KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; AAC67491.

XX

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 931 AA;

Query Match 85.9%; Score 249; DB 7; Length 931;
Best Local Similarity 82.0%; Pred. No. 1.1e-19;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50

|||||||||:: ||||:|||:||:|||||||||:||| || |||

Db 264 STWTEWSVCNSRCGRGYQKRTRCTNPAPLNGGAFCEGQSVQKIACTTLC 313

Search completed: March 1, 2005, 08:56:47
Job time : 11.4389 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:42:47 ; Search time 2.99591 Seconds
(without alignments)
1245.848 Million cell updates/sec

Title: US-10-624-932-2_COPY_246_295

Perfect score: 290

Sequence: 1 STWTEWSVCSASCGRGWQKR.....NGGAFCEGQNVQKTACATLC 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Query Score	Match	Length	DB	ID	Description
1	290	100.0	898	2	US-08-808-982-5	Sequence 5, Appli
2	290	100.0	898	3	US-09-306-902A-5	Sequence 5, Appli
3	249	85.9	769	4	US-09-949-016-10665	Sequence 10665, A
4	238	82.1	943	2	US-08-808-982-7	Sequence 7, Appli
5	238	82.1	943	3	US-09-306-902A-7	Sequence 7, Appli
6	147	50.7	939	4	US-09-854-845-16	Sequence 16, Appli
7	147	50.7	954	4	US-09-854-845-14	Sequence 14, Appli
8	147	50.7	1034	4	US-09-854-845-6	Sequence 6, Appli
9	147	50.7	1049	4	US-09-854-845-2	Sequence 2, Appli
10	147	50.7	1078	4	US-09-854-845-8	Sequence 8, Appli
11	147	50.7	1093	4	US-09-854-845-4	Sequence 4, Appli

12	147	50.7	1136	4	US-09-854-845-12	Sequence 12, Appl
13	147	50.7	1151	4	US-09-854-845-10	Sequence 10, Appl
14	139	47.9	1224	4	US-09-930-872-4	Sequence 4, Appli
15	139	47.9	1224	4	US-10-217-774-4	Sequence 4, Appli
16	137	47.2	584	1	US-08-313-288B-17	Sequence 17, Appl
17	136	46.9	479	4	US-09-270-767-46823	Sequence 46823, A
18	136	46.9	481	4	US-09-130-491-8	Sequence 8, Appli
19	132	45.5	239	5	PCT-US93-01652-1	Sequence 1, Appli
20	132	45.5	837	4	US-09-122-126B-2	Sequence 2, Appli
21	132	45.5	837	4	US-09-634-286A-2	Sequence 2, Appli
22	132	45.5	837	4	US-10-247-685-2	Sequence 2, Appli
23	132	45.5	1170	4	US-09-657-472-2	Sequence 2, Appli
24	131	45.2	905	3	US-09-369-364A-9	Sequence 9, Appli
25	130	44.8	551	4	US-09-130-491-16	Sequence 16, Appl
26	130	44.8	608	4	US-09-130-491-13	Sequence 13, Appl
27	130	44.8	727	4	US-09-445-023A-1	Sequence 1, Appli
28	130	44.8	727	4	US-09-445-023A-12	Sequence 12, Appl
29	130	44.8	949	4	US-09-568-559-2	Sequence 2, Appli
30	130	44.8	950	4	US-09-321-987B-4	Sequence 4, Appli
31	130	44.8	967	4	US-09-130-491-2	Sequence 2, Appli
32	128.5	44.3	950	4	US-10-009-332-1	Sequence 1, Appli
33	128	44.1	1170	1	US-08-313-288B-20	Sequence 20, Appl
34	126	43.4	2150	4	US-09-321-987B-2	Sequence 2, Appli
35	126	43.4	2165	4	US-09-800-729-155	Sequence 155, App
36	122	42.1	321	4	US-09-969-532-24	Sequence 24, Appl
37	122	42.1	332	4	US-09-969-532-22	Sequence 22, Appl
38	122	42.1	335	4	US-09-969-532-20	Sequence 20, Appl
39	122	42.1	346	4	US-09-969-532-18	Sequence 18, Appl
40	122	42.1	552	4	US-09-969-532-8	Sequence 8, Appli
41	122	42.1	563	4	US-09-969-532-6	Sequence 6, Appli
42	122	42.1	566	4	US-09-969-532-4	Sequence 4, Appli
43	122	42.1	577	4	US-09-969-532-2	Sequence 2, Appli
44	122	42.1	655	4	US-09-969-532-32	Sequence 32, Appl
45	122	42.1	666	4	US-09-969-532-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
 US-08-808-982-5
 ; Sequence 5, Application US/08808982
 ; Patent No. 5939271
 ; GENERAL INFORMATION:
 ; APPLICANT: Tessier-Lavigne, Marc
 ; APPLICANT: Leonardo, E. David
 ; APPLICANT: Hink, Lindsay
 ; APPLICANT: Masu, Masayuki
 ; APPLICANT: Kazuko, Keino-Masu
 ; TITLE OF INVENTION: Netrin Receptors
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA

ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,982
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-808-982-5

```

Query Match           100.0%;  Score 290;  DB 2;  Length 898;
Best Local Similarity 100.0%;  Pred. No. 3.6e-25;
Matches 50;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||| |
Db      246 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 295

```

RESULT 2

US-09-306-902A-5
; Sequence 5, Application U
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier
; ; Leonard
; ; Hink, L
; ; Masu, M
; ; Kazuko,
; TITLE OF INVENTION
; NUMBER OF SEQUENCE
; CORRESPONDENCE ADDRESS
; ADDRESSEE: SC
; STREET: 268 B
; CITY: SAN FRA
; STATE: CALIFO
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE
; MEDIUM TYPE:
; COMPUTER: IBM

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/306,902A
FILING DATE: 07-May-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-306-902A-5

RESULT 3

US-09-949-016-10665

; Sequence 10665, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES

THEOREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/2

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/2

; PRIOR FILING DATE: 2000-09-08 .

; NUMBER OF SEQ ID NOS: 207012

; SEQ ID NO 10665

; LENGTH: 769

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-10665

Query Match 85.9%; Score 249; DB 4; Length 769;
Best Local Similarity 82.0%; Pred. No. 1.5e-20;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 102 STWTEWSVCNSRCGRGYQKRRTCTNPAPLNGGAFCEGQSVQKIACATLC 151

RESULT 4

US-08-808-982-7

; Sequence 7, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/808,982

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 943 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

US-08-808-982-7

Query Match 82.1%; Score 238; DB 2; Length 943;
Best Local Similarity 78.0%; Pred. No. 3.4e-19;
Matches 39; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
|:| ||| || |||||||||:|:||||||||| ||| ||| |:|
Db 248 SSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQACQKTACTTVC 297

RESULT 5

US-09-306-902A-7

; Sequence 7, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 943 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-306-902A-7

Query Match 82.1%; Score 238; DB 3; Length 943;
Best Local Similarity 78.0%; Pred. No. 3.4e-19;
Matches 39; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
|:| ||| || |||||||||:|:||||||||| ||| ||| |:|

Db

248 SSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQACQKTACTTVC 297

RESULT 6

US-09-854-845-16
; Sequence 16, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 939
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-16

Query Match 50.7%; Score 147; DB 4; Length 939;
Best Local Similarity 54.2%; Pred. No. 9.1e-09;
Matches 26; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT 48
| || || || || || | :|:|||:||| | | | | : :: |||
Db 717 SCWTSWSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEALCAT 764

RESULT 7

US-09-854-845-14
; Sequence 14, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 954
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-14

Query Match 50.7%; Score 147; DB 4; Length 954;
Best Local Similarity 54.2%; Pred. No. 9.2e-09;
Matches 26; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT 48
| || || || || || || | :|:|||:||| | | | : :: |||
Db 717 SCWTWSWSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEALCAT 764

RESULT 8

US-09-854-845-6

; Sequence 6, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-6

Query Match 50.7%; Score 147; DB 4; Length 1034;
Best Local Similarity 54.2%; Pred. No. 1e-08;
Matches 26; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT 48
| || || || || || | :|:|||:||| | | | : :: |||
Db 812 SCWTWSWSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEALCAT 859

RESULT 9

US-09-854-845-2

; Sequence 2, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade

; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-2

Query Match 50.7%; Score 147; DB 4; Length 1049;
Best Local Similarity 54.2%; Pred. No. 1e-08;
Matches 26; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACAT 48
| || || || || || | :|:|||:||| | | | : :: |||
Db 812 SCWTWSWSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEEALCAT 859

RESULT 10
US-09-854-845-8
; Sequence 8, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-8

Query Match 50.7%; Score 147; DB 4; Length 1078;
Best Local Similarity 54.2%; Pred. No. 1e-08;

Matches 26; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT 48
| || || || || || | :|:|||:||| | | | : :: |||
Db 856 SCWTWSWSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEEALCAT 903

RESULT 11

US-09-854-845-4

; Sequence 4, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845.
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1093
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-4

Query Match 50.7%; Score 147; DB 4; Length 1093;
Best Local Similarity 54.2%; Pred. No. 1.1e-08;
Matches 26; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT 48
| || || || || || | :|:|||:||| | | | : :: |||
Db 856 SCWTWSWSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEEALCAT 903

RESULT 12

US-09-854-845-12

; Sequence 12, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274

; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1136
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-12

Query Match 50.7%; Score 147; DB 4; Length 1136;
Best Local Similarity 54.2%; Pred. No. 1.1e-08;
Matches 26; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1. STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT 48
| || || ||||||| | :|||:||| | | | | : :: |||
Db 914 SCWTSWSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEALCAT 961

RESULT 13
US-09-854-845-10
; Sequence 10, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-10

Query Match 50.7%; Score 147; DB 4; Length 1151;
Best Local Similarity 54.2%; Pred. No. 1.1e-08;
Matches 26; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACAT 48
| || || ||||||| | :|||:||| | | | | : :: |||
Db 914 SCWTSWSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEALCAT 961

RESULT 14
US-09-930-872-4

; Sequence 4, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/09/930,872
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1224
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-930-872-4

Query Match 47.9%; Score 139; DB 4; Length 1224;
Best Local Similarity 52.0%; Pred. No. 9.8e-08;
Matches 26; Conservative 3; Mismatches 17; Indels 4; Gaps 1;

QY 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
| |: || || :|| | ||| |||| | :|| |||| | |||
Db 590 SDWSSWSPCSRTCAGGVSHRSRLCTNPKPSSHGGKFCEG----STRTLKLC 635

RESULT 15
US-10-217-774-4
; Sequence 4, Application US/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6734007el Human Proteases and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1224
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-217-774-4

Query Match 47.9%; Score 139; DB 4; Length 1224;
Best Local Similarity 52.0%; Pred. No. 9.8e-08;
Matches 26; Conservative 3; Mismatches 17; Indels 4; Gaps 1;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
| |: || || :|| | | || || || | :|| || || | | ||
Db 590 SDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCEG----STRTLKLC 635

Search completed: March 1, 2005, 09:05:52
Job time : 3.99591 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:46:18 ; Search time 1.95188 Seconds
(without alignments)
2464.715 Million cell updates/sec

Title: US-10-624-932-2_COPY_246_295

Perfect score: 290

Sequence: 1 STWTEWSVCSASCGRGWQKR.....NGGAFCEGQNVQKTACATLC 50

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	148	51.0	1074	2	JC5928	semaphorin F precu
2	138	47.6	584	1	C8HUA	complement C8 alph
3	132	45.5	837	2	T00355	hypothetical prote
4	130.5	45.0	1444	2	T18856	angiogenesis inhib
5	130	44.8	550	2	T47158	hypothetical prote
6	130	44.8	951	2	T00017	gene ADAMTS-1 prot
7	128	44.1	1170	1	TSHUP1	thrombospondin 1 p
8	127	43.8	919	2	T32541	unc-5 protein - Ca
9	127	43.8	947	1	B44294	unc-5 protein, lon
10	126	43.4	1170	2	A40558	thrombospondin 1 p
11	126	43.4	2165	2	T21371	hypothetical prote
12	123	42.4	585	2	I46686	complement compone
13	119	41.0	1572	2	T00027	brain-specific ang

14	119	41.0	1584	2	T00026	brain-specific ang
15	118.5	40.9	437	2	S05478	properdin - mouse
16	118	40.7	254	2	T15952	hypothetical prote
17	117	40.3	654	2	T29247	hypothetical prote
18	116.5	40.2	984	2	T00326	hypothetical prote
19	116.5	40.2	1522	2	T00028	brain-specific ang
20	115	39.7	1178	1	A39804	thrombospondin pre
21	113.5	39.1	469	1	S29126	properdin precurso
22	111.5	38.4	934	1	A34372	complement C6 prec
23	110	37.9	1172	1	TSHUP2	thrombospondin 2 p
24	109.5	37.8	957	2	T15976	hypothetical prote
25	109	37.6	1172	2	A42587	thrombospondin 2 p
26	108	37.2	788	2	T25061	hypothetical prote
27	106	36.6	590	2	I46687	complement compone
28	106	36.6	843	1	A27340	complement C7 prec
29	104	35.9	1205	2	T18517	procollagen N-endo
30	99.5	34.3	805	2	T34212	hypothetical prote
31	96	33.1	860	2	T16892	hypothetical prote
32	94	32.4	591	1	C8HUB	complement C8 beta
33	92	31.7	2761	2	T21064	hypothetical prote
34	91	31.4	206	2	A45517	coccidiosis-relate
35	91	31.4	712	2	A45638	immunodominant mic
36	91	31.4	736	2	T19366	hypothetical prote
37	90	31.0	807	2	A38152	F-spondin - rat
38	89	30.7	803	2	A47723	F-spondin precurso
39	89	30.7	1360	2	T33922	hypothetical prote
40	86.5	29.8	610	2	T16761	hypothetical prote
41	86.5	29.8	1184	2	T09484	cartilage intermed
42	84	29.0	898	2	T14764	hypothetical prote
43	84	29.0	1059	2	T22545	hypothetical prote
44	80	27.6	651	2	T19477	hypothetical prote
45	79	27.2	724	2	A48569	antigen Em100 - Ei

ALIGNMENTS

RESULT 1

JC5928

Semaphorin F precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: JC5928

R;Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M. Biochem. Biophys. Res. Commun. 242, 685-691, 1998

A;Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-chat candidate interval.

A;Reference number: JC5928; MUID:98125554; PMID:9464278

A;Accession: JC5928

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1074 <SIM>

A;Cross-references: UNIPROT:Q13591; GB:U52840; NID:g2772583; PIDN: AAC09473.1; PID:g2772584

A;Experimental source: brain

C;Comment: This protein disrupts normal brain development and leads to some of the features of Cri-du-chat.

C;Genetics:
A;Gene: semaf
C;Superfamily: human semaphorin F; thrombospondin type 1 repeat homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;50-533/Domain: semaphorin #status predicted <SEM>
F;840-896/Domain: thrombospondin type 1 repeat homology <THR3>
F;971-993/Domain: transmembrane #status predicted <TMM>

Query Match 51.0%; Score 148; DB 2; Length 1074;
Best Local Similarity 54.5%; Pred. No. 6.6e-09;
Matches 24; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
|| || || :|| |:| | |||:|| | :|| | ||| :: |
Db 601 WTSWSPCSTTCGIGFQVRQRSCSNPTRHGGRVCVGQNRREERYC 644

RESULT 2

C8HUA

complement C8 alpha chain precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000
C;Accession: I37213; A26704
R;Michelotti, G.A.; Snider, J.V.; Sodetz, J.M.
Hum. Genet. 95, 513-518, 1995
A;Title: Genomic organization of human complement protein C8 alpha and further examination of its linkage to C8 beta.
A;Reference number: I37213; MUID:95278905; PMID:7759071
A;Accession: I37213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-584 <MIC>
A;Cross-references: EMBL:U08006; NID:g901862; PIDN:AAA82124.1; PID:g901864
R;Rao, A.G.; Howard, O.M.Z.; Ng, S.C.; Whitehead, A.S.; Colten, H.R.; Sodetz, J.M.
Biochemistry 26, 3556-3564, 1987
A;Title: Complementary DNA and derived amino acid sequence of the alpha subunit of human complement protein C8: evidence for the existence of a separate alpha subunit messenger RNA.
A;Reference number: A26704; MUID:88000560; PMID:2820471
A;Accession: A26704
A;Molecule type: mRNA
A;Residues: 1-92, 'Q', 94-466, 'CCGTQAWASGGQ', 480-574, 'P', 576-584 <RAO>
A;Note: part of the sequence was confirmed by protein sequencing
R;Hofsteenge, J.; Blommers, M.; Hess, D.; Furmanek, A.; Miroshnichenko, O. J. Biol. Chem. 274, 32786-32794, 1999
A;Title: The four terminal components of the complement system are C-mannosylated on multiple tryptophan residues.
A;Reference number: A59362; MUID:20020247; PMID:10551839
A;Contents: annotation
A;Note: identification and location of C-mannosylation sites by mass-spectroscopy
C;Genetics:
A;Gene: GDB:C8A
A;Cross-references: GDB:119735; OMIM:120950
A;Map position: 1p32-1p32
A;Introns: 26/2; 57/3; 106/1; 155/2; 218/3; 285/3; 366/1; 408/1; 460/3; 535/1

C;Complex: heterotrimer of C8 alpha chain (PIR:C8HUA), C8 beta chain (PIR:C8HUB), and C8 gamma chain (PIR:C8HUG); the trimer associates with the C5b-7 complex
C;Function:
A;Description: combines with complement C5b-7 complex to polymerize complement component C9
A;Pathway: complement pathway
C;Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology; thrombospondin type 1 repeat homology
C;Keywords: complement pathway; cytolysis; glycoprotein; membrane attack complex; plasma
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-30/Domain: propeptide #status predicted <PRO>
F;31-584/Product: complement C8 alpha chain #status predicted <MPT>
F;37-91/Domain: thrombospondin type 1 repeat homology <THR1>
F;96-130/Domain: LDL receptor ligand-binding repeat homology <LDL>
F;497-528/Domain: EGF homology <EGF>
F;538-584/Domain: thrombospondin type 1 repeat homology <THR2>
F;43/Binding site: carbohydrate (Asn) (covalent) #status absent
F;44,542,545,548/Modified site: 2'-mannosyl-tryptophan (Trp) #status experimental
F;437/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.6%; Score 138; DB 1; Length 584;
Best Local Similarity 56.5%; Pred. No. 5.3e-08;
Matches 26; Conservative 3; Mismatches 13; Indels 4; Gaps 1;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
| |: |||| | | | |: | | | | ||| | |: || ||
Db 543 SCWSSWSVCRA----GIQERRRECDNPAPQNGGASCSGRKVQTQAC 584

RESULT 3

T00355

hypothetical protein KIAA0688 - human

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C;Accession: T00355

R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.

DNA Res. 5, 169-176, 1998

A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.

A;Reference number: Z14142; MUID:98403880; PMID:9734811

A;Accession: T00355

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-837 <ISH>

A;Cross-references: UNIPROT:O75173; EMBL:AB014588; NID:g3327189; PIDN:BAA31663.1; PID:g3327190

A;Experimental source: brain

C;Genetics:

A;Gene: KIAA0688

F;519-575/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 45.5%; Score 132; DB 2; Length 837;

Best Local Similarity 47.8%; Pred. No. 3.4e-07;
Matches 22; Conservative. 5; Mismatches 19; Indels 0; Gaps 0;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACAT 48
| | | || :|| | | || | | | || :||: : :| |
Db 526 WGPWGDCSRTCGGGVQFSSRDCTRVPVRNGGKYCEGRRTRFRSCNT 571

RESULT 4

T18856

angiogenesis inhibitor homolog - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T18856; T24653

R;McMurray, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19031

A;Accession: T18856

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1444 <WIL>

A;Cross-references: UNIPROT:Q8MYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028;

CESP:C02B4.1

A;Experimental source: clone C02B4

R;McMurray, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19917

A;Accession: T24653

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1444 <WI2>

A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1

A;Experimental source: clone T07C5

C;Genetics:

A;Gene: CESP:C02B4.1

A;Map position: X

A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3;
509/3; 566/2; 625/1; 696/2; 786/3; 812/2; 878/3; 971/1; 1007/3; 1067/1; 1099/3;
1180/3; 1273/2; 1305/1; 1363/1; 1388/2

Query Match 45.0%; Score 130.5; DB 2; Length 1444;

Best Local Similarity 52.2%; Pred. No. 7.8e-07;

Matches 24; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46

|||:||: ||||| | | | |||:|| | || | | | | : |

Db 1311 STWSDWTPCSASCGRGWQTRDRSCSSPEP-KGGQSCSGLAHQTS 1355

RESULT 5

T47158

hypothetical protein DKFZp762C1110.1 - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: T47158

R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.

submitted to the Protein Sequence Database, March 2000

A;Reference number: Z24379
A;Accession: T47158
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-550 <AAA>
A;Cross-references: UNIPROT:Q9UHI8; EMBL:AL162080
A;Experimental source: adult melanoma (MeWo cell line); clone DKFZp762C1110
C;Genetics:
A;Note: DKFZp762C1110.1

Query Match 44.8%; Score 130; DB 2; Length 550;
Best Local Similarity 47.7%; Pred. No. 4e-07;
Matches 21; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
| | || :|| || | | || | || :||: |: :|
Db 148 WGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSC 191

RESULT 6
T00017
gene ADAMTS-1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 15-Mar-2004
C;Accession: T00017
R;Kuno, K.; Lizasa, H.; Ohno, S.; Matsushima, K.
Genomics 46, 466-471, 1997
A;Title: The exon/intron organization and chromosomal mapping of the mouse
ADAMTS-1 gene encoding an ADAM family protein with TSP motifs.
A;Reference number: Z14055; MUID:98110583; PMID:9441751
A;Accession: T00017
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-951 <KUN>
A;Cross-references: EMBL:AB001735; NID:g2809056; PIDN:BAA24501.1; PID:g2809057
A;Experimental source: strain 129SVJ
C;Genetics:
A;Gene: ADAMTS-1
A;Introns: 228/1; 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2
F;542-598/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 44.8%; Score 130; DB 2; Length 951;
Best Local Similarity 47.7%; Pred. No. 6.3e-07;
Matches 21; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
| | || :|| || | | || | || :||: |: :|
Db 549 WGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSC 592

RESULT 7
TSHUP1
thrombospondin 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A26155; A34274; A30140; A25812; A05172; A42927
R;Lawler, J.; Hynes, R.O.

J. Cell Biol. 103, 1635-1648, 1986

A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different proteins.

A;Reference number: A26155; MUID:87057617; PMID:2430973

A;Accession: A26155

A;Molecule type: mRNA

A;Residues: 1-1170 <LAW>

A;Cross-references: UNIPROT:P07996; GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138

A;Note: parts of this sequence, including the amino end of the mature protein, were determined by protein sequencing

R;Laherty, C.D.; Gierman, T.M.; Dixit, V.M.

J. Biol. Chem. 264, 11222-11227, 1989

A;Title: Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.

A;Reference number: A34274; MUID:89291870; PMID:2544587

A;Accession: A34274

A;Molecule type: DNA

A;Residues: 1-166 <LAH>

A;Cross-references: GB:J04835

R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, P.; Frazier, W.A.

J. Cell Biol. 108, 729-736, 1989

A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region.

A;Reference number: A30140; MUID:89139590; PMID:2918029

A;Accession: A30140

A;Molecule type: mRNA

A;Residues: 1-83,'A',85-522,'A',524-1170 <HEN>

A;Cross-references: EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID:g37465

A;Note: parts of this sequence, including the amino end of the mature protein, were determined by protein sequencing

R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.

Biochemistry 25, 8418-8425, 1986

A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite proteins.

A;Reference number: A25812; MUID:87157592; PMID:3030396

A;Accession: A25812

A;Molecule type: mRNA

A;Residues: 1-83,'A',85-397 <KOB>

A;Cross-references: GB:M25631; NID:g538353; PIDN:AAA36741.1; PID:g538354

R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.

Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986

A;Reference number: A05172; MUID:86287276; PMID:3461443

A;Accession: A05172

A;Molecule type: mRNA

A;Residues: 1-83,'A',85-374,'RC' <DIX>

A;Cross-references: GB:M14326; NID:g340005; PIDN:AAA61237.1; PID:g553801

A;Note: parts of this sequence, including the amino end of the mature protein, were determined by protein sequencing

R;Sun, X.; Skorstengaard, K.; Mosher, D.F.

J. Cell Biol. 118, 693-701, 1992

A;Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.

A;Reference number: A42927; MUID:92348511; PMID:1379247

A;Accession: A42927

A;Molecule type: protein

A;Residues: 987-1003 <SUN>
A;Note: Cys-992 is shown to have a free sulfhydryl
C;Genetics:
A;Gene: GDB:THBS1; TSP1; TSP
A;Cross-references: GDB:120438; OMIM:188060
A;Map position: 15q15-15q15
A;Introns: 23/1
A;Note: the list of introns may be incomplete
C;Complex: homotrimer, disulfide linked
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F;551-586/Domain: EGF homology <EGF1>
F;650-689/Domain: EGF homology <EGF2>
F;926-928/Region: cell attachment (R-G-D) motif
F;171-232/Disulfide bonds: #status predicted
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;270,274/Disulfide bonds: interchain #status predicted
F;610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 44.1%; Score 128; DB 1; Length 1170;
Best Local Similarity 47.7%; Pred. No. 1.2e-06;
Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
|: | :|| :|| | ||||| | ||| | || | | : |
Db 498 WSPWDICSVTCGGGVQKRSRLCNNPTPQFGGKDCVGDVTEENQIC 541

RESULT 8
T32541
unc-5 protein - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32541
R;Latreille, P.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of *C. elegans* cosmid B0273.
A;Reference number: Z21187
A;Accession: T32541
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-919 <LAT>
A;Cross-references: UNIPROT:O44171; EMBL:AF036698; PIDN:AAB88355.1;
GSPDB:GN00022; CESP:B0273.4a
A;Experimental source: strain Bristol N2; clone B0273

C;Genetics:
A;Gene: unc-5; CESP:B0273.4a
A;Map position: 4
A;Introns: 41/3; 108/1; 142/3; 201/1; 323/2; 553/1; 858/3
C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; thombospondin type 1 repeat homology

Query Match 43.8%; Score 127; DB 2; Length 919;
Best Local Similarity 47.1%; Pred. No. 1.3e-06;
Matches 24; Conservative 9; Mismatches 14; Indels 4; Gaps 2;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC-ATLC 50
|:|::|| ||:|| | |:|:|| |:||| | |:: | | |||
Db 278 SSWSDWSACSSSCHR--YRTRACTVPPPMNGGQPCFGDDLMTQECPAQLC 325

RESULT 9
B44294
unc-5 protein, long form - *Caenorhabditis elegans*
N;Contains: unc-5 protein, short form
C;Species: *Caenorhabditis elegans*
C;Date: 30-Apr-1993 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C;Accession: B44294; T32540; A44294
R;Leung-Hagesteijn, C.; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.; Hedgecock, E.M.; Culotti, J.G.
Cell 71, 289-299, 1992
A;Title: UNC-5, a transmembrane protein with immunoglobulin and thombospondin type 1 domains, guides cell and pioneer axon migrations in *C. elegans*.
A;Reference number: A44294; MUID:93046629; PMID:1384987
A;Contents: variety Bergerac
A;Accession: B44294
A;Molecule type: DNA
A;Residues: 1-947 <LEU>
A;Cross-references: UNIPROT:O44171; GB:S47168; NID:g258527; PIDN:AAB23867.1; PID:g258529
A;Note: sequence extracted from NCBI backbone (NCBIN:116668, NCBIN:116670, NCBIN:116672, NCBIN:116674, NCBIN:116676, NCBIN:116678, NCBIN:116680, NCBIN:116682, NCBIN:116685, NCBIP:118648)
A;Note: authors translated the codon CTA for residue 642 as Val; sequence shown follows the authors' translation
A;Note: mRNA lacking the first exon is equally prevalent
R;Latreille, P.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of *C. elegans* cosmid B0273.
A;Reference number: Z21187
A;Accession: T32540
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-947 <LAT>
A;Cross-references: EMBL:AF036698; PIDN:AAB88356.1; GSPDB:GN00022; CESP:B0273.4b
A;Experimental source: strain Bristol N2; clone B0273
C;Genetics:
A;Gene: unc-5
A;Map position: 4
A;Introns: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3
C;Function:

A;Description: required for guidance of pioneering axons and cells migrating dorsally along the body wall; proposed to be a receptor on the surface of the motile cells
C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; thrombospondin type 1 repeat homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein
F;30-947/Product: unc-5 protein, short form #status predicted <ALT>
F;46-116/Domain: immunoglobulin homology <IM1>
F;153-211/Domain: immunoglobulin homology <IM2>
F;229-300/Domain: thrombospondin type 1 repeat homology #status atypical <THR1>
F;301-354/Domain: thrombospondin type 1 repeat homology <THR2>
F;365-390/Domain: transmembrane #status predicted <TMM>
F;512-559/Domain: SH3 homology <SH3>
F;53-114,65-112,160-209/Disulfide bonds: #status predicted
F;206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.8%; Score 127; DB 1; Length 947;
Best Local Similarity 47.1%; Pred. No. 1.4e-06;
Matches 24; Conservative 9; Mismatches 14; Indels 4; Gaps 2;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC-ATLC 50
|:|::|| ||:|| | |:||:|| |:||| | |:: | | ||
Db 306 SSWSDWSACSSSCHR--YRTRACTVPPPMNGQPCFGDDLMTQECPAQLC 353

RESULT 10

A40558

thrombospondin 1 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004

C;Accession: A40558; A37905; B42587; S68787

R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.

Genomics 11, 587-600, 1991

A;Title: Characterization of the murine thrombospondin gene.

A;Reference number: A40558; MUID:92128941; PMID:1774063

A;Accession: A40558

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1170 <LAW>

A;Cross-references: UNIPROT:P35441; GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453; GB:M62454; GB:M62455; GB:M62456; GB:M62457; GB:M62458; GB:M62459; GB:M62460; GB:M62461; GB:M62462; GB:M62463; GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:g511867; PIDN:AAA50611.1; PID:g511869

R;Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P. J. Biol. Chem. 265, 16691-16698, 1990

A;Title: Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.

A;Reference number: A37905; MUID:90375546; PMID:2398070

A;Accession: A37905

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-490 <BOR>

A;Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390

R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression
during cell growth and development.
A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: B42587
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1152,'P',1154-1170 <LAH>
A;Cross-references: GB:M87276
A;Note: sequence extracted from NCBI backbone (NCBIP:81501)
R;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse
thrombospondin 1 and thrombospondin 3.
A;Reference number: S68787; MUID:96234006; PMID:8654563
A;Accession: S68787
A;Molecule type: protein
A;Residues: 19-26,'X',28-37 <CHE>
C;Complex: homotrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat
homology; von Willebrand factor type C repeat homology
C;Keywords: calcium binding; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F;551-586/Domain: EGF homology <EGF>
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.4%; Score 126; DB 2; Length 1170;
Best Local Similarity 45.5%; Pred. No. 2.1e-06;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
|: | :|| :|| | :|| | || | || | | : |
Db 498 WSPWDICSVTCGGGVQRRSRLCNNPTPQFGGKDCVGDVTENQVC 541

RESULT 11
T21371
hypothetical protein F25H8.3 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21371; T24896
R;Gajadsty, S.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19413
A;Accession: T21371
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2165 <WIL>
A;Cross-references: UNIPROT:Q19791; EMBL:Z69360; PIDN:CAA93287.1; GSPDB:GN00022;
CESP:F25H8.3
A;Experimental source: clone F25H8

R;Gajadsty, S.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19949
A;Accession: T24896
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2165 <WI2>
A;Cross-references: EMBL:Z69361; PIDN:CAA93288.1; GSPDB:GN00022; CESP:F25H8.3
A;Experimental source: clone T13H10
C;Genetics:
A;Gene: CESP:F25H8.3
A;Map position: 4
A;Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2;
744/1; 814/1; 961/2; 1251/3; 1338/3; 1500/3; 1553/3; 1647/3; 1704/3; 1762/3;
1820/3; 1938/1; 1998/2; 2044/1; 2109/3

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Query Match           43.4%;  Score 126;  DB 2;  Length 2165;
Best Local Similarity 45.7%;  Pred. No. 3.5e-06;
Matches 21;  Conservative 5;  Mismatches 20;  Indels 0;  Gaps 0;

Qy      3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACAT 48
       || || || : || | || | | : | || | : | || : : | |
Db      609 WRSWGECRSRTCGGGVOKGLRDCDSPKPRNGGKYCVGORERYRSCNT 654

```

RESULT 12

T46686

complement component C8 alpha subunit - rabbit

C; Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 14-Feb-1997 #sequence revision 14-Feb-1997 #text change 09-Jul-2004

C:Accession: T46686

R;White, R.V.; Kaufman, K.M.; Letson, C.S.; Platteborze, P.L.; Sodetz, J.M.
J. Immunol. 152, 2501-2508, 1994

A;Title: Characterization of rab).

for the species-selective recognition of C8 alpha by homologous restriction factor (CD59).

A; Reference number: I46686; MUID: 94179833; PMID: 7510745

A:Accession: I46686

A;Status: preliminary; translated from GB/EMBL/DDBJ

A: Molecule type: mRNA

A; Residues: 1-585 <WHI>

A;Cross-references: UNIPROT:P98136; GB:L26981; NID:g469060; PIDN:AAA31191.1;
PID:g469061

C; Superfamily: complement C9; EGF homology; LDL receptor ligand

homology; thrombospondin type 1 repeat homology

F;37-91/Domain: thrombospondin type

RESULT 13
T00027
brain-specific angiogenesis inhibitor 2 - human
N;Alternate names: BAI2 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00027
R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cytogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-specific angiogenesis inhibitor 1 (BAI 1).
A;Reference number: Z14066; MUID:98194217; PMID:9533023
A;Accession: T00027
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1572 <SHI>
A;Cross-references: UNIPROT:O60241; EMBL:AB005298; NID:g3021698;
PIDN:BAA25362.1; PID:g3021699
A;Experimental source: brain
C;Genetics:
A;Gene: GDB:BAI2
A;Cross-references: GDB:9838089; OMIM:602683
A;Map position: 1p35-1p35

Query Match 41.0%; Score 119; DB 2; Length 1572;
Best Local Similarity 46.7%; Pred. No. 1.6e-05;
Matches 21; Conservative 6; Mismatches 16; Indels 2; Gaps 1;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGAFCEGQNVQKTACA 47
| ||:|| ||||| : | |:| | :|| || :| |:
Db 358 WGSWSLCSRSCGRGSRSRMRTCV--PPQHGGKACEGPELQTKLCS 400

RESULT 14
T00026
brain-specific angiogenesis inhibitor 1 - human
N;Alternate names: BAI1 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00026
R;Nishimori, H.; Shiratsuchi, T.; Urano, T.; Kimura, Y.; Kiyono, K.; Tatsumi, K.; Yoshida, S.; Ono, M.; Kuwano, M.; Nakamura, Y.
submitted to the EMBL Data Library, June 1997
A;Reference number: Z14064
A;Accession: T00026
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1584 <NIS>
A;Cross-references: UNIPROT:O14514; EMBL:AB005297; NID:d1175078; PID:d1024528
A;Experimental source: brain
C;Genetics:
A;Gene: GDB:BAI1
A;Cross-references: GDB:9838088; OMIM:602682
A;Map position: 8q24-8q24
F;408-462/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 41.0%; Score 119; DB 2; Length 1584;
Best Local Similarity 47.7%; Pred. No. 1.6e-05;
Matches 21; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
|: || |||| :| :||:| | |: ||| |:| |: |
Db 473 WSSWSACSASC SQGRQRTRECNGPS--YGGAECQGHWVETRDC 514

RESULT 15

S05478

properdin - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: S05478

R;Goundis, D.; Reid, K.B.M.

Nature 335, 82-85, 1988

A;Title: Properdin, the terminal complement components, thrombospondin and the circumsporozoite protein of malaria parasites contain similar sequence motifs.

A;Reference number: S05478; MUID:88318954; PMID:3045564

A;Accession: S05478

A;Molecule type: mRNA

A;Residues: 1-437 <GOU>

A;Cross-references: UNIPROT:P11680; EMBL:X12905; NID:g53786; PIDN:CAA31389.1; PID:g53787

C;Complex: a mixture of homodimers, homotrimers and homotetramers

C;Function:

A;Description: protects C3 convertase (C3bBb) from rapid inactivation

A;Pathway: complement alternate pathway

C;Superfamily: human properdin precursor; thrombospondin type 1 repeat homology

C;Keywords: complement alternate pathway; glycoprotein; homodimer; homotetramer; homotrimer; plasma

F;45-97/Domain: thrombospondin type 1 repeat homology <THR1>

F;104-160/Domain: thrombospondin type 1 repeat homology <THR2>

F;161-224/Domain: thrombospondin type 1 repeat homology <THR3>

F;225-282/Domain: thrombospondin type 1 repeat homology <THR4>

F;283-345/Domain: thrombospondin type 1 repeat homology <THR5>

F;346-408/Domain: thrombospondin type 1 repeat homology <THR6>

F;52,55,108,111,114,165,168,229,232,290,293,350,353,356/Modified site: 2'-mannosyl-tryptophan (Trp) #status predicted

F;366,396/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.9%; Score 118.5; DB 2; Length 437;

Best Local Similarity 47.9%; Pred. No. 6.4e-06;

Matches 23; Conservative 3; Mismatches 21; Indels 1; Gaps 1;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACAT 48

| | | || :| :|| | | | | ||| | | | |: | | | |

Db 109 SEWGPWGPCSVTCSKGTQIRQRVCDNPAPKCGG-HCPGEAQQSQACDT 155

Search completed: March 1, 2005, 09:07:20

Job time : 2.95188 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2005, 09:06:01 ; Search time 9.62324 Seconds
(without alignments)
1704.439 Million cell updates/sec

Title: US-10-624-932-2_COPY_246_295

Perfect score: 290

Sequence: 1 STWTEWSVCSASCGRGWQKR.....NGGAFCEGQNVQKTACATLC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	290	100.0	898	10	US-09-933-261-5	Sequence 5, Appli
2	290	100.0	898	10	US-09-918-779-2	Sequence 2, Appli
3	290	100.0	898	10	US-09-970-944-13	Sequence 13, Appli
4	290	100.0	898	14	US-10-256-702-5	Sequence 5, Appli
5	290	100.0	898	14	US-10-240-154-16	Sequence 16, Appli
6	290	100.0	898	15	US-10-624-932-2	Sequence 2, Appli
7	249	85.9	931	10	US-09-970-944-15	Sequence 15, Appli
8	249	85.9	931	10	US-09-970-944-16	Sequence 16, Appli
9	249	85.9	931	10	US-09-970-944-17	Sequence 17, Appli
10	249	85.9	931	11	US-09-972-211-121	Sequence 121, App
11	249	85.9	931	11	US-09-972-211-122	Sequence 122, App
12	249	85.9	931	11	US-09-972-211-125	Sequence 125, App
13	249	85.9	931	15	US-10-087-684-35	Sequence 35, Appli
14	249	85.9	931	15	US-10-087-684-36	Sequence 36, Appli
15	249	85.9	931	15	US-10-218-779-36	Sequence 36, Appli
16	249	85.9	931	15	US-10-037-417-117	Sequence 117, App
17	249	85.9	931	15	US-10-037-417-118	Sequence 118, App
18	249	85.9	931	15	US-10-037-417-119	Sequence 119, App
19	249	85.9	931	15	US-10-037-417-120	Sequence 120, App
20	249	85.9	931	15	US-10-096-625-121	Sequence 121, App
21	249	85.9	931	15	US-10-096-625-122	Sequence 122, App
22	249	85.9	931	15	US-10-096-625-125	Sequence 125, App
23	249	85.9	1010	15	US-10-218-779-35	Sequence 35, Appli
24	243	83.8	899	10	US-09-970-944-2	Sequence 2, Appli
25	239	82.4	56	17	US-10-872-681-32	Sequence 32, Appli
26	239	82.4	679	15	US-10-094-886-118	Sequence 118, App
27	239	82.4	887	17	US-10-872-681-54	Sequence 54, Appli
28	239	82.4	924	16	US-10-473-518-63	Sequence 63, Appli
29	239	82.4	933	15	US-10-087-684-2	Sequence 2, Appli
30	239	82.4	933	15	US-10-087-684-4	Sequence 4, Appli
31	239	82.4	933	15	US-10-218-779-2	Sequence 2, Appli
32	239	82.4	933	15	US-10-218-779-4	Sequence 4, Appli
33	239	82.4	945	14	US-10-028-072-146	Sequence 146, App
34	239	82.4	945	14	US-10-140-808-146	Sequence 146, App
35	239	82.4	945	14	US-10-121-049-146	Sequence 146, App
36	239	82.4	945	14	US-10-123-904-146	Sequence 146, App
37	239	82.4	945	14	US-10-140-470-146	Sequence 146, App
38	239	82.4	945	14	US-10-175-746-146	Sequence 146, App
39	239	82.4	945	14	US-10-176-918-146	Sequence 146, App
40	239	82.4	945	14	US-10-176-921-146	Sequence 146, App
41	239	82.4	945	14	US-10-137-865-146	Sequence 146, App
42	239	82.4	945	14	US-10-140-474-146	Sequence 146, App
43	239	82.4	945	14	US-10-142-431-146	Sequence 146, App
44	239	82.4	945	14	US-10-143-114-146	Sequence 146, App
45	239	82.4	945	14	US-10-142-419-146	Sequence 146, App

ALIGNMENTS

RESULT 1
 US-09-933-261-5
 ; Sequence 5, Application US/09933261

; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030040046A1 Relevant
; TOPOLOGY: No. US20030040046A1 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-933-261-5

Query Match 100.0%; Score 290; DB 10; Length 898;
Best Local Similarity 100.0%; Pred. No. 9.9e-24;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
Db 246 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 295

RESULT 2
US-09-918-779-2
; Sequence 2, Application US/09918779

; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-918-779-2

;
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
;
; COUNTRY: USA
;
; ZIP: 94104
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/10/256,702
;
; FILING DATE: 27-Sep-2002
;
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/933,261
;
; FILING DATE: 20-Aug-2001
;
; APPLICATION NUMBER: 08/808,982
;
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: OSMAN, RICHARD A
;
; REGISTRATION NUMBER: 36,627
;
; REFERENCE/DOCKET NUMBER: UC96-217
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (415) 343-4341
;
; TELEFAX: (415) 343-4342
;
; INFORMATION FOR SEQ ID NO: 5:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 898 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: No. US20030059859A1 Relevant
;
; TOPOLOGY: No. US20030059859A1 Relevant
;
; MOLECULE TYPE: peptide
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-256-702-5

Query Match 100.0%; Score 290; DB 14; Length 898;
Best Local Similarity 100.0%; Pred. No. 9.9e-24;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
Db 246 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 295

RESULT 5

US-10-240-154-16
;
; Sequence 16, Application US/10240154
;
; Publication No. US20030175741A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Cochran et al.
;
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
;
; FILE REFERENCE: CKFW-P01-006
;
; CURRENT APPLICATION NUMBER: US/10/240,154
;
; CURRENT FILING DATE: 2001-04-02
;
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
;
; PRIOR FILING DATE: 2001-04-02
;
; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-240-154-16

Query Match 100.0%; Score 290; DB 14; Length 898;
Best Local Similarity 100.0%; Pred. No. 9.9e-24;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STWTEWSVCASACGRGWQKRSRSCTNPAPLNGGAFCEQNVQKTACATLC 50
Db 246 STWTEWSVCASACGRGWQKRSRSCTNPAPLNGGAFCEQNVQKTACATLC 295

RESULT 6

US-10-624-932-2

; Sequence 2, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/0
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,710
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,400
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,810
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,710
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,710
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,710
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,710

RESULT 8
US-09-970-944-16
; Sequence 16, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1 e Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-970-944-16

US-09-970-944-16

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Query Match          85.9%;  Score 249;  DB 10;  Length 931;
Best Local Similarity 82.0%;  Pred. No. 3.5e-19;
Matches 41;  Conservative 6;  Mismatches 3;  Indels 0;  Gaps 0;

Y 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
|||:|||||:: ||||:|||:||:|||||:|||||:|||  ||  |||  |
D 264 STWTEWSVCNSRCGRGYQKRRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

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RESULT 9

US-09-970-944-17

; Sequence 17, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 931
; TYPE: PRT
; ORGANISM: *Caenorhabditis elegans*
US-09-970-944-17

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Query Match           85.9%;  Score 249;  DB 10;  Length 931;
Best Local Similarity 82.0%;  Pred. No. 3.5e-19;
Matches   41;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy      1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
        |||||||::: ||||:|||:||:|||||:|||||:|||  ||  |||  |
Db      264 STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

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RESULT 10

US-09-972-211-121

; Sequence 121, Application US/09972211

; Publication No. US20040048245A1

GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennda
; APPLICANT: Szekeres Jr, Edward S

; TITLE OF INVENTION: No. US20040048245A1 Human Proteins, Polynucleotides
Encoding Them And

; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384

; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 931
; TYPE: PRT
; ORGANISM: *Mus musculus*
US-09-972-211-121

US-09-972-211-121

Query Match 85.9%; Score 249; DB 11; Length 931;
Best Local Similarity 82.0%; Pred. No. 3.5e-19;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATL 50
|||:|||||:::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 264 STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTL 313

RESULT 11
US-09-972-211-122
; Sequence 122, Application US/0997221
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennda
; APPLICANT: Szekeres Jr, Edward S

; TITLE OF INVENTION: No. US20040048245A1 Human Proteins, Polynucleotides
Encoding Them And
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-211-122

Query Match 85.9%; Score 249; DB 11; Length 931;
Best Local Similarity 82.0%; Pred. No. 3.5e-19;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
|||:|||||:: ||||:|||:||:|||||||||:||| || |||
Db 264 STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACATLC 313

RESULT 12
US-09-972-211-125
; Sequence 125, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A

; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennda
; APPLICANT: Szekeres Jr, Edward S
; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides
Encoding Them And
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125

; LENGTH: 931
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-211-125

Query Match 85.9%; Score 249; DB 11; Length 931;
Best Local Similarity 82.0%; Pred. No. 3.5e-19;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
|||:|||||:: ||||:|||:|:|||||:|||||:||| |||
Db 264 STWTEWSVCNSRCGRGYQKRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

RESULT 13

US-10-087-684-35

; Sequence 35, Application US/10087684

; Publication No. US20040029116A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Cathereine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.

; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-214 CIP

; CURRENT APPLICATION NUMBER: US/10/087,684

; CURRENT FILING DATE: 2003-03-10

; PRIOR APPLICATION NUMBER: 60/253,834

; PRIOR FILING DATE: 2000-11-29

; PRIOR APPLICATION NUMBER: 60/250,926

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: 60/264,180

; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: 60/274,194

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 60/313,656

; PRIOR FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 35
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-684-35

Query Match 85.9%; Score 249; DB 15; Length 931;
Best Local Similarity 82.0%; Pred. No. 3.5e-19;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 1 STWTEWSVCASCGRGWQKRSRCTNPAPLNGGAFCEGQNVQKTACATLC 50
Db 264 STWTEWSVCNSRCGRGYQKRTRCTNPAPLNGGAFCEGQSVQKIACTTLC 313

RESULT 14

US-10-087-684-36

; Sequence 36, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Cathereine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaoqia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180

; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 36
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-684-36

Query Match 85.9%; Score 249; DB 15; Length 931;
Best Local Similarity 82.0%; Pred. No. 3.5e-19;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
|||:|||||:: ||||:|||:|:|||||||||:||| || |||
Db 264 STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

RESULT 15

US-10-218-779-36

; Sequence 36, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Paturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaoqia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-36

Query Match 85.9%; Score 249; DB 15; Length 931;
Best Local Similarity 82.0%; Pred. No. 3.5e-19;
Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 264 STWTEWSVCNSRCGRGYQKRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

Search completed: March 1, 2005, 09:51:30
Job time : 9.62324 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:41:47 ; Search time 9.14662 Seconds
(without alignments)
2799.282 Million cell updates/sec

Title: US-10-624-932-2_COPY_246_295

Perfect score: 290

Sequence: 1 STWTEWSVCSASCGRGWQKR.....NGGAFCEGQNVQKTACATLC 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	290	100.0	898	1	UN5A_MOUSE	Q8k1s4 mus musculu
2	290	100.0	898	1	UN5A_RAT	O08721 rattus norv
3	249	85.9	931	1	UN5C_CHICK	Q7t2z5 gallus gall
4	249	85.9	931	1	UN5C_HUMAN	O95185 homo sapien
5	249	85.9	931	1	UN5C_MOUSE	O08747 mus musculu
6	244	84.1	931	1	UN5C_RAT	Q761x5 rattus norv
7	239	82.4	945	1	UN5B_HUMAN	Q8izj1 homo sapien
8	239	82.4	953	1	UN5D_HUMAN	Q6uxz4 homo sapien
9	238	82.1	945	1	UN5B_MOUSE	Q8k1s3 mus musculu
10	238	82.1	945	1	UN5B_RAT	O08722 rattus norv
11	238	82.1	956	1	UN5D_MOUSE	Q8k1s2 mus musculu
12	219	75.5	943	1	UN5B_XENLA	Q8jgt4 xenopus lae
13	148	51.0	335	2	Q8BVQ2	Q8bvq2 m mus muscu
14	148	51.0	844	2	Q8BXU8	Q8bxu8 m mus muscu
15	148	51.0	1074	1	SM5A_HUMAN	Q13591 homo sapien

16	148	51.0	1077	1	SM5A_MOUSE	Q62217	mus musculu
17	147	50.7	1092	2	Q6UY12	Q6uy12	homo sapien
18	147	50.7	1093	1	SM5B_HUMAN	Q9p283	homo sapien
19	147	50.7	1151	2	Q6DD89	Q6dd89	homo sapien
20	144	49.7	1388	2	Q7QKD0	Q7qkd0	anopheles g
21	143	49.3	478	2	Q8BVE5	Q8bve5	m mus muscu
22	143	49.3	632	2	Q6ZPQ8	Q6zpq8	mus musculu
23	143	49.3	1088	2	Q6PCK8	Q6pck8	xenopus lae
24	143	49.3	1093	1	SM5B_MOUSE	Q60519	mus musculu
25	143	49.3	1122	2	Q7TT33	Q7tt33	mus musculu
26	143	49.3	1244	2	Q69YJ3	Q69yj3	homo sapien
27	143	49.3	2673	2	Q96SC3	Q96sc3	homo sapien
28	143	49.3	5636	2	Q96RW7	Q96rw7	homo sapien
29	139	47.9	1224	1	AT16_HUMAN	Q8te57	homo sapien
30	138.5	47.8	4998	2	Q8CG65	Q8cg65	mus musculu
31	137	47.2	584	1	CO8A_HUMAN	P07357	homo sapien
32	136	46.9	769	2	Q8MRL5	Q8mrl5	drosophila
33	136	46.9	839	2	Q7YS95	Q7ys95	bos taurus
34	136	46.9	1059	2	Q9W493	Q9w493	drosophila
35	136	46.9	1081	2	Q9U631	Q9u631	drosophila
36	136	46.9	1091	2	Q7YU67	Q7yu67	drosophila
37	136	46.9	1093	2	Q9VTT0	Q9vtt0	drosophila
38	135.5	46.7	5141	2	Q700K0	Q700k0	rattus norv
39	132.5	45.7	1072	1	UNC5_DROME	Q95tu8	drosophila
40	132	45.5	833	2	Q8K384	Q8k384	mus musculu
41	132	45.5	837	1	ATS4_HUMAN	Q75173	homo sapien
42	132	45.5	837	2	Q6UWA8	Q6uwa8	homo sapien
43	132	45.5	845	2	Q8BNJ2	Q8bnj2	mus musculu
44	132	45.5	893	2	Q6A017	Q6a017	mus musculu
45	131	45.2	900	2	Q8K206	Q8k206	mus musculu

ALIGNMENTS

RESULT 1

UN5A_MOUSE

ID UN5A_MOUSE STANDARD; PRT; 898 AA.

AC Q8K1S4; Q6PEF7; Q80T71;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).

GN Name=Unc5a; Synonyms=Kiaal1976, Unc5h1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.

RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;

RA Engelkamp D.;

RT "Cloning of three mouse unc-5 genes and their expression patterns at mid-gestation.";

RL Mech. Dev. 118:191-197(2002).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand (By
CC similarity).
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
CC with MAGED1. Interacts with PRKCABP, possibly mediating some
CC interaction with PKC (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
CC with PRKCABP regulates its surface expression and leads to its
CC removal from surface of neurons and growth cones (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q8K1S4-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8K1S4-2; Sequence=VSP_011697;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q8K1S4-3; Sequence=VSP_011696;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Restricted to central nervous system.

CC --!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis (By similarity).
 CC --!- PTM: Phosphorylated by PKC in vitro. Phosphorylated on cytoplasmic
 CC tyrosine residues (By similarity).
 CC --!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC --!- SIMILARITY: Belongs to the UNC-5 family.
 CC --!- SIMILARITY: Contains 1 death domain.
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC --!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC --!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ487852; CAD32250.1; -.
 DR EMBL; AK122575; BAC65857.1; ALT_INIT.
 DR EMBL; BC058084; AAH58084.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:894682; Unc5a.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PRO1705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 898 Netrin receptor UNC5A.
 FT DOMAIN 26 361 Extracellular (Potential).
 FT TRANSMEM 362 382 Potential.
 FT DOMAIN 383 898 Cytoplasmic (Potential).
 FT DOMAIN 44 141 Ig-like.
 FT DOMAIN 155 234 Ig-like C2-type.

FT	DOMAIN	242	296	TSP type-1 1.
FT	DOMAIN	298	350	TSP type-1 2.
FT	DOMAIN	495	598	ZU5.
FT	DOMAIN	817	897	Death.
FT	SITE	396	397	Cleavage (by caspase-3) (By similarity).
FT	SITE	661	679	Interaction with DCC (By similarity).
FT	DISULFID	65	124	By similarity.
FT	DISULFID	170	221	By similarity.
FT	CARBOHYD	107	107	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	218	218	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	343	343	N-linked (GlcNAc. . .) (Potential).
FT	VARSPPLIC	1	790	Missing (in isoform 3).
FT				/FTId=VSP_011696.
FT	VARSPPLIC	241	296	Missing (in isoform 2).
FT				/FTId=VSP_011697.
FT	CONFLICT	217	217	A -> P (in Ref. 3).
SQ	SEQUENCE	898 AA;	98856 MW;	59F04BA2E196C1DB CRC64;

Query Match 100.0%; Score 290; DB 1; Length 898;
 Best Local Similarity 100.0%; Pred. No. 8.2e-26;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
 |||||||
 Db 246 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 295

RESULT 2

UN5A_RAT

ID UN5A_RAT STANDARD; PRT; 898 AA.
 AC 008721;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
 GN Name=Unc5a; Synonyms=Unc5h1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Ventral spinal cord;
 RX MEDLINE=97271897; PubMed=9126742;
 RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
 RA Tessier-Lavigne M.;
 RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin
 receptors.";
 RL Nature 386:833-838(1997).
 RN [2]
 RP FUNCTION, AND INTERACTION WITH DCC.
 RX PubMed=10399920;
 RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
 RA Stein E.;
 RT "A ligand-gated association between cytoplasmic domains of UNC5 and
 RT DCC family receptors converts netrin-induced growth cone attraction to

RT repulsion.";
RL Cell 97:927-941(1999).
RN [3]
RP TISSUE SPECIFICITY.
RX PubMed=11472849;
RA Barrett C., Guthrie S.;
RT "Expression patterns of the netrin receptor UNC5H1 among developing
RT motor neurons in the embryonic rat hindbrain.";
RL Mech. Dev. 106:163-166(2001).
RN [4]
RP FUNCTION.
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
RL EMBO J. 20:2715-2722(2001).
RN [5]
RP FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH MAGED1.
RX PubMed=12598531; DOI=10.1074/jbc.M300415200;
RA Williams M.E., Strickland P., Watanabe K., Hinck L.;
RT "UNC5H1 induces apoptosis via its juxtamembrane region through an
RT interaction with NRAGE.";
RL J. Biol. Chem. 278:17483-17490(2003).
RN [6]
RP INTERACTION WITH PRKCABP, PHOSPHORYLATION, AND MUTAGENESIS OF
RP 896-ALA--CYS-898.
RX PubMed=14672991; DOI=23/36/11279;
RA Williams M.E., Wu S.C.-Y., McKenna W.L., Hinck L.;
RT "Surface expression of the netrin receptor UNC5H1 is regulated through
RT a protein kinase C-interacting protein/protein kinase-dependent
RT mechanism.";
RL J. Neurosci. 23:11279-11288(2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand.
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
CC with MAGED1. Interacts with PRKCABP, possibly mediating some
CC interaction with PKC.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
CC with PRKCABP regulates its surface expression and leads to its
CC removal from surface of neurons and growth cones.
CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
CC neurons. Expressed at early stages of neural tube development in
CC the ventral spinal cord. In developing hindbrain, it colocalizes
CC with a number of cranial motor neuron subpopulations from
CC embryonic E11 to E14, while DCC is expressed by motor neurons at
CC E12. Also expressed in non-neuronal structures, such as the basal
CC plane of the hindbrain and midbrain, in the developing
CC hypothalamus, thalamus and in the pallidium.
CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
CC participates in the induction of apoptosis.
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity). Phosphorylated by PKC in vitro.
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with

CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC --!- SIMILARITY: Belongs to the UNC-5 family.
 CC --!- SIMILARITY: Contains 1 death domain.
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC --!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC --!- SIMILARITY: Contains 1 ZU5 domain.
 CC

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 CC

 DR EMBL; U87305; AAB57678.1; -.
 DR HSSP; P07996; 1LSL.
 DR RGD; 621755; Unc5h1.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PRO1705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 898 Netrin receptor UNC5A.
 FT DOMAIN 26 361 Extracellular (Potential).
 FT TRANSMEM 362 382 Potential.
 FT DOMAIN 383 898 Cytoplasmic (Potential).
 FT DOMAIN 44 141 Ig-like.
 FT DOMAIN 155 238 Ig-like C2-type.
 FT DOMAIN 242 296 TSP type-1 1.
 FT DOMAIN 298 350 TSP type-1 2.
 FT DOMAIN 495 598 ZU5.
 FT DOMAIN 817 897 Death.
 FT SITE 396 397 Cleavage (by caspase-3) (By similarity).
 FT SITE 661 679 Interaction with DCC (By similarity).
 FT DISULFID 65 124 By similarity.
 FT DISULFID 170 221 By similarity.
 FT CARBOHYD 107 107 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 218 218 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 343 343 N-linked (GlcNAc. . .) (Potential).
 FT MUTAGEN 896 898 Missing: Abolishes interaction with PRKCABP.
 FT SQ SEQUENCE 898 AA; 98840 MW; 7A3CBCB9E7ACA135 CRC64;
 Query Match 100.0%; Score 290; DB 1; Length 898;
 Best Local Similarity 100.0%; Pred. No. 8.2e-26;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
 |||||||
 Db 246 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 295
 RESULT 3
 UN5C_CHICK
 ID UN5C_CHICK STANDARD; PRT; 931 AA.
 AC Q7T2Z5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
 DE (cUNC-5H3).
 GN Name=UNC5C;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX PubMed=12799087;
 RA Guan W., Condic M.L.;
 RT "Characterization of Netrin-1, Neogenin and cUNC-5H3 expression during
 RT chick dorsal root ganglia development.";
 RL Gene Expr. Patterns 3:369-373(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Restricted to proprioceptive neurons.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC
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 CC
 DR EMBL; AY187310; AAO67275.1; -.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Developmental protein; Immunoglobulin domain; Phosphorylation;
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 39 Potential.
 FT CHAIN 40 931 Netrin receptor UNC5C.
 FT DOMAIN 40 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 931 Cytoplasmic (Potential).
 FT DOMAIN 62 159 Ig-like.
 FT DOMAIN 161 256 Ig-like C2-type.
 FT DOMAIN 260 314 TSP type-1 1.
 FT DOMAIN 316 368 TSP type-1 2.
 FT DOMAIN 528 631 ZU5.
 FT DOMAIN 850 929 Death.
 FT DISULFID 83 142 By similarity.
 FT DISULFID 188 239 By similarity.
 FT CARBOHYD 236 236 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 931 AA; 102906 MW; 1E23A0D84F2E2C62 CRC64;

Query Match 85.9%; Score 249; DB 1; Length 931;
 Best Local Similarity 82.0%; Pred. No. 6.1e-21;
 Matches 41; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
 ||||||| ||:: ||||:|||:||:|||||||||||||||||| || |||
 Db 264 STWTEWSACNSRCGRGFQKRTCTNPAPLNGGAFCEGQNVQKIACTTLC 313

RESULT 4
 UN5C_HUMAN
 ID UN5C_HUMAN STANDARD; PRT; 931 AA.
 AC 095185; Q8IUT0;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).
 GN Name=UNC5C; Synonyms=UNC5H3;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=99000841; PubMed=9782087; DOI=10.1006/geno.1998.5425;
RA Ackerman S.L., Knowles B.B.;
RT "Cloning and mapping of the UNC5C gene to human chromosome 4q21-q23.";
RL Genomics 52:205-208(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP DOWN-REGULATION IN CANCER.
RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
RT "The netrin-1 receptors UNC5H are putative tumor suppressors
RT controlling cell death commitment.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. Also involved in corticospinal tract axon guidances
CC independently of DCC. It also acts as a dependence receptor
CC required for apoptosis induction when not associated with netrin
CC ligand (By similarity).
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=095185-1; Sequence=Displayed;

CC Name=2;
CC IsoId=O95185-2; Sequence=VSP_011700, VSP_011701;
CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in
CC kidney. Not expressed in developing or adult lung.
CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
CC phosphatase, suggesting that its activity is regulated by
CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
CC netrin-dependent (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis (By similarity).
CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
CC cancers.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----
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CC -----
DR EMBL; AF055634; AAC67491.1; -.
DR EMBL; BC041156; AAH41156.1; -.
DR HSSP; P07996; 1LSL.
DR Genew; HGNC:12569; UNC5C.
DR MIM; 603610; -.
DR GO; GO:0005042; F:netrin receptor activity; TAS.
DR GO; GO:0007411; P:axon guidance; TAS.
DR GO; GO:0007420; P:brain development; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PRO1705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.

DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 40 Potential.
 FT CHAIN 41 931 Netrin receptor UNC5C.
 FT DOMAIN 41 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 931 Cytoplasmic (Potential).
 FT DOMAIN 62 159 Ig-like.
 FT DOMAIN 161 256 Ig-like C2-type.
 FT DOMAIN 260 314 TSP type-1 1.
 FT DOMAIN 316 368 TSP type-1 2.
 FT DOMAIN 528 631 ZU5.
 FT DOMAIN 850 929 Death.
 FT SITE 415 416 Cleavage (by caspase-3) (By similarity).
 FT SITE 694 712 Interaction with DCC (By similarity).
 FT DISULFID 83 142 By similarity.
 FT DISULFID 188 239 By similarity.
 FT MOD_RES 568 568 Phosphotyrosine (By similarity).
 FT CARBOHYD 236 236 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 370 370 T -> SFIYPISTEQRTQNEYGFSS (in isoform 2).
 FT /FTId=VSP_011700.
 FT VARSPLIC 579 931 Missing (in isoform 2).
 FT /FTId=VSP_011701.
 FT VARIANT 37 37 G -> V (in dbSNP:2306715).
 FT /FTId=VAR_019731.
 FT VARIANT 721 721 T -> M (in dbSNP:2289043).
 FT /FTId=VAR_019732.
 FT CONFLICT 219 219 T -> I (in Ref. 1).
 FT CONFLICT 489 489 S -> T (in Ref. 1).
 SQ SEQUENCE 931 AA; 103101 MW; EFD71122C98DABB8 CRC64;

Query Match 85.9%; Score 249; DB 1; Length 931;
 Best Local Similarity 82.0%; Pred. No. 6.1e-21;
 Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
 |||||||::: ||||:||:||:||||||||||||:||| |||
 Db 264 STWTEWSVCNSRCGRGYQKRTRCTNPAPLNGGAFCEGQSVQKIACTTLC 313

RESULT 5
 UN5C_MOUSE
 ID UN5C_MOUSE STANDARD; PRT; 931 AA.
 AC O08747; Q8CD16;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
 DE (Rostral cerebellar malformation protein).
 GN Name=Unc5c; Synonyms=Rcm, Unc5h3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, DISEASE, AND TISSUE
RP SPECIFICITY.
RC STRAIN=C57B6/SJL;
RX MEDLINE=97271898; PubMed=9126743;
RA Ackerman S.L., Kozak L.P., Przyborski S.A., Rund L.A., Boyer B.B.,
RA Knowles B.B.;
RT "The mouse rostral cerebellar malformation gene encodes an UNC-5-like
RT protein.";
RL Nature 386:838-842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=9389662;
RA Przyborski S.A., Knowles B.B., Ackerman S.L.;
RT "Embryonic phenotype of Unc5h3 mutant mice suggests chemorepulsion
RT during the formation of the rostral cerebellar boundary.";
RL Development 125:41-50(1998).
RN [4]
RP INTERACTION WITH DCC.
RX PubMed=10399920;
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
RA Stein E.;
RT "A ligand-gated association between cytoplasmic domains of UNC5 and
RT DCC family receptors converts netrin-induced growth cone attraction to

RT repulsion.";
RL Cell 97:927-941(1999).
RN [5]
RP PHOSPHORYLATION SITE TYR-568, AND MUTAGENESIS OF TYR-568.
RX PubMed=11533026; DOI=10.1074/jbc.M103872200;
RA Tong J., Killeen M., Steven R., Binns K.L., Culotti J., Pawson T.;
RT "Netrin stimulates tyrosine phosphorylation of the UNC-5 family of
RT netrin receptors and induces Shp2 binding to the RCM cytodomain.";
RL J. Biol. Chem. 276:40917-40925(2001).
RN [6]
RP FUNCTION.
RX PubMed=12451134; DOI=22/23/10346;
RA Finger J.H., Bronson R.T., Harris B., Johnson K., Przyborski S.A.,
RA Ackerman S.L.;
RT "The netrin 1 receptors Unc5h3 and Dcc are necessary at multiple
RT choice points for the guidance of corticospinal tract axons.";
RL J. Neurosci. 22:10346-10356(2002).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. Also involved in corticospinal tract axon guidances
CC independently of DCC. It also acts as a dependence receptor
CC required for apoptosis induction when not associated with netrin
CC ligand.
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=008747-1; Sequence=Displayed;
CC Name=2;
CC IsoId=008747-2; Sequence=VSP_011702;
CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
CC neurons. Highly expressed in brain and lung. Weakly expressed in
CC testis, ovary, spleen, thymus and bladder. Expressed at very low
CC level in kidney, intestine and salivary gland.
CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
CC phosphatase, suggesting that its activity is regulated by
CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
CC netrin-dependent.
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis (By similarity).
CC -!- DISEASE: Defects in Unc5c are the cause of rostral cerebellar
CC malformation (Rcm). Rcm is characterized by cerebellar and
CC midbrain defects, apparently as a result of abnormal neuronal
CC migration.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----

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CC -----

DR EMBL; U72634; AAB54103.1; -.
DR EMBL; AK031655; BAC27495.1; -.
DR HSSP; P07996; 1LSL.
DR MGD; MGI:1095412; Unc5c.
DR GO; GO:0005886; C:plasma membrane; IC.
DR GO; GO:0005042; F:netrin receptor activity; IDA.
DR GO; GO:0005515; F:protein binding; IDA.
DR GO; GO:0007420; P:brain development; IMP.
DR GO; GO:0030334; P:regulation of cell migration; IMP.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Alternative splicing; Apoptosis; Developmental protein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 40 Potential.
FT CHAIN 41 931 Netrin receptor UNC5C.
FT DOMAIN 41 380 Extracellular (Potential).
FT TRANSMEM 381 401 Potential.
FT DOMAIN 402 931 Cytoplasmic (Potential).
FT DOMAIN 62 159 Ig-like.
FT DOMAIN 161 256 Ig-like C2-type.
FT DOMAIN 260 314 TSP type-1 1.
FT DOMAIN 316 368 TSP type-1 2.
FT DOMAIN 528 631 ZU5.
FT DOMAIN 850 929 Death.
FT SITE 415 416 Cleavage (by caspase-3) (By similarity).
FT SITE 694 712 Interaction with DCC (By similarity).
FT DISULFID 83 142 By similarity.
FT DISULFID 188 239 By similarity.
FT MOD_RES 568 568 Phosphotyrosine.
FT CARBOHYD 236 236 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 361 361 N-linked (GlcNAc. . .) (Potential).

FT VARSPLIC 370 370 A -> GFIYPISTEHRPQNEYGFSS (in isoform 2).
 FT /FTId=VSP_011702.
 FT MUTAGEN 568 568 Y->F: Abolishes interaction with PTPN11,
 FT leading to a increased level of
 FT phosphorylation.
 FT CONFLICT 16 16 L -> I (in Ref. 2).
 FT CONFLICT 733 733 H -> R (in Ref. 2).
 FT CONFLICT 924 924 S -> Y (in Ref. 2).
 SQ SEQUENCE 931 AA; 103062 MW; 8A5D951A4EECA179 CRC64;

 Query Match 85.9%; Score 249; DB 1; Length 931;
 Best Local Similarity 82.0%; Pred. No. 6.1e-21;
 Matches 41; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 STWTEWSVCASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
 |||||||:: ||||:||:||:|||||||||:||| || |||
 Db 264 STWTEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

RESULT 6

UN5C_RAT

ID UN5C_RAT STANDARD; PRT; 931 AA.
 AC Q761X5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).
 GN Name=Unc5c; Synonyms=Unc5h3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND DISEASE.
 RX PubMed=15010202; DOI=10.1016/j.molbrainres.2003.12.003;
 RA Kuramoto T., Kuwamura M., Serikawa T.;
 RT "Rat neurological mutations cerebellar vermis defect and hobble are
 caused by mutations in the netrin-1 receptor gene Unc5h3.";
 RL Brain Res. Mol. Brain Res. 122:103-108 (2004).
 RN [2]
 RP FUNCTION.
 RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
 RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
 RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
 RL EMBO J. 20:2715-2722 (2001).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in

CC kidney. Not expressed in developing or adult lung.
CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
CC phosphatase, suggesting that its activity is regulated by
CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
CC netrin-dependent (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis.
CC -!- DISEASE: Defects in Unc5c are the cause of cerebellar vermis
CC défect (cvd) and hobble (hob) phenotypes. Cvd and hob rats exhibit
CC cerebellar and midbrain defects, possibly as a result of abnormal
CC neuronal migration, and exhibit laminar structure abnormalities in
CC the fused cerebellar hemispheres and ectopic cerebellar tissues in
CC the cerebello-pontine junction.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC

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CC or send an email to license@isb-sib.ch).
CC

DR EMBL; AB118026; BAD05181.1; -.
DR RGD; 735109; Unc5c.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PRO1705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Apoptosis; Developmental protein; Immunoglobulin domain;
KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 40 Potential.

FT CHAIN 41 931 Netrin receptor UNC5C.
 FT DOMAIN 41 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 931 Cytoplasmic (Potential).
 FT DOMAIN 62 159 Ig-like.
 FT DOMAIN 161 256 Ig-like C2-type.
 FT DOMAIN 260 314 TSP type-1 1.
 FT DOMAIN 316 368 TSP type-1 2.
 FT DOMAIN 528 631 ZU5.
 FT DOMAIN 850 929 Death.
 FT SITE 415 416 Cleavage (by caspase-3) (By similarity).
 FT SITE 694 712 Interaction with DCC (By similarity).
 FT DISULFID 83 142 By similarity.
 FT DISULFID 188 239 By similarity.
 FT MOD_RES 568 568 Phosphotyrosine (By similarity).
 FT CARBOHYD 236 236 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 931 AA; 103134 MW; 25B183A97BCB8401 CRC64;

Query Match 84.1%; Score 244; DB 1; Length 931;
 Best Local Similarity 80.0%; Pred. No. 2.4e-20;
 Matches 40; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
 |||| |||||:: ||||:||:||:|||||||||||||:||| || |||
 Db 264 STWAEWSVCNSRCGRGYQKRTRTCTNPAPLNGGAFCEGQSVQKIACTTLC 313

RESULT 7

UN5B_HUMAN

ID UN5B_HUMAN STANDARD; PRT; 945 AA.
 AC Q8IZJ1; Q86SN3; Q8N1Y2; Q9H9F3;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2)
 DE (p53-regulated receptor for death and life protein 1)
 DE (UNQ1883/PRO4326).
 GN Name=UNC5B; Synonyms=P53RDL1, UNC5H2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION
 RP WITH GNAI2.
 RC TISSUE=Lung;
 RX MEDLINE=22246081; PubMed=12359238; DOI=10.1016/S0006-291X(02)02277-5;
 RA Komatsuzaki K., Dalvin S., Kinane T.B.;
 RT "Modulation of G(ialpha(2)) signaling by the axonal guidance molecule
 RT UNC5H2.";
 RL Biochem. Biophys. Res. Commun. 297:898-905(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND MUTAGENESIS OF ASP-412.
 RX PubMed=12598906; DOI=10.1038/ncb943;
 RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
 RT "p53RDL1 regulates of p53-dependent apoptosis.";

RL Nat. Cell Biol. 5:216-223(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE OF 361-945 FROM N.A.
RC TISSUE=Amygdala, and Teratocarcinoma;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togoya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [5]
RP DOWN-REGULATION IN CANCER.
RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;

RT "The netrin-1 receptors UNC5H are putative tumor suppressors controlling cell death commitment.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178 (2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates axon repulsion of neuronal growth cones in the developing nervous system upon ligand binding. Axon repulsion in growth cones may be caused by its association with DCC that may trigger signaling for repulsion. It also acts as a dependence receptor required for apoptosis induction when not associated with netrin ligand.
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By similarity). Interacts with GNAI2 via its cytoplasmic part.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8IZJ1-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8IZJ1-2; Sequence=VSP_011698;
CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed at lower level in developing lung, cartilage, kidney and hematopoietic and immune tissues.
CC -!- INDUCTION: By p53/TP53.
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The cleavage does not take place when the receptor is associated with netrin ligand. Its cleavage by caspases is required to induce apoptosis.
CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including colorectal, breast, ovary, uterus, stomach, lung, or kidney cancers.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----
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CC -----
DR EMBL; AY126437; AAM95701.1; -.
DR EMBL; AB096256; BAC57998.1; -.
DR EMBL; AY358351; AAQ88717.1; -.
DR EMBL; AK022859; BAB14276.1; ALT_INIT.
DR EMBL; AK094595; BAC04382.1; ALT_INIT.
DR HSSP; P07996; 1LSL.
DR Genew; HGNC:12568; UNC5B.
DR MIM; 607870; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PRO1705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 945 Netrin receptor UNC5B.
 FT DOMAIN 27 377 Extracellular (Potential).
 FT TRANSMEM 378 398 Potential.
 FT DOMAIN 399 945 Cytoplasmic (Potential).
 FT DOMAIN 48 145 Ig-like.
 FT DOMAIN 147 242 Ig-like C2-type.
 FT DOMAIN 246 300 TSP type-1 1.
 FT DOMAIN 302 354 TSP type-1 2.
 FT DOMAIN 541 644 ZU5.
 FT DOMAIN 865 943 Death.
 FT SITE 412 413 Cleavage (by caspase-3).
 FT SITE 707 725 Interaction with DCC (By similarity).
 FT DISULFID 69 128 By similarity.
 FT DISULFID 174 225 By similarity.
 FT CARBOHYD 222 222 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 356 367 NKKTLSDPNSHL -> M (in isoform 2).
 FT /FTId=VSP_011698.
 FT VARIANT 516 516 A -> T (in dbSNP:10509332).
 FT /FTId=VAR_019730.
 FT MUTAGEN 412 412 D->N: Abolishes cleavage by caspase-3 and
 FT subsequent induction of apoptosis.
 FT CONFLICT 483 483 K -> E (in Ref. 3).
 FT CONFLICT 851 851 L -> P (in Ref. 3; BAB14276).
 SQ SEQUENCE 945 AA; 103637 MW; 56064E335F323447 CRC64;

 Query Match 82.4%; Score 239; DB 1; Length 945;
 Best Local Similarity 78.0%; Pred. No. 9.4e-20;
 Matches 39; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

 Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
 |:| ||| || .|||||||:|:||||||| ||||| :|:
 Db 250 SSWAEWSPCSNRCGRGWQKRTCTNPAPLNGGAFCEGQAFQKTACTTIC 299

RESULT 8
 UN5D_HUMAN

ID UN5D_HUMAN STANDARD; PRT; 953 AA.
AC Q6UXZ4; Q8WYP7;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4)
DE (UNQ6012/PRO34692).
GN Name=UNC5D; Synonyms=KIAA1777, UNC5H4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270 (2003).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RA Nakajima D., Nakayama M., Nagase T., Ohara O.;
RT "Identification of unc5H4 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Receptor for netrin. May be involved in axon guidance by
CC mediating axon repulsion of neuronal growth cones in the
CC developing nervous system upon ligand binding. Axon repulsion in
CC growth cones may be caused by its association with DCC that may
CC trigger signaling for repulsion. It also acts as a dependence
CC receptor required for apoptosis induction when not associated with
CC netrin ligand (By similarity).
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q6UXZ4-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q6UXZ4-2; Sequence=VSP_011703;
CC Note=No experimental confirmation available;
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis (By similarity).

CC --!- SIMILARITY: Belongs to the UNC-5 family.
 CC --!- SIMILARITY: Contains 1 death domain.
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC --!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC --!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AB055056; BAB83663.1; -.
 DR EMBL; AY358147; AAQ88514.1; -.
 DR HSSP; P07996; 1LSL.
 DR Genew; HGNC:18634; UNC5D.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 953 Netrin receptor UNC5D.
 FT DOMAIN 33 379 Extracellular (Potential).
 FT TRANSMEM 380 400 Potential.
 FT DOMAIN 401 953 Cytoplasmic (Potential).
 FT DOMAIN 54 151 Ig-like.
 FT DOMAIN 153 244 Ig-like C2-type.
 FT DOMAIN 252 306 TSP type-1 1.
 FT DOMAIN 308 360 TSP type-1 2.
 FT DOMAIN 540 642 ZU5.
 FT DOMAIN 859 936 Death.
 FT SITE 416 417 Cleavage (by caspase-3) (By similarity).
 FT SITE 703 721 Interaction with DCC (By similarity).
 FT DISULFID 75 134 By similarity.
 FT DISULFID 180 231 By similarity.
 FT CARBOHYD 117 117 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 228 228 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 353 353 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 376 376 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 1 34 MGRAAATAGGGGGARRWLPWLGLCFWAAGTAAAR -> MIL
 FT VLVKALSDVCAGTSGFLLDFSSQTSP (in isoform
 2).
 FT /FTId=VSP_011703.
 SQ SEQUENCE 953 AA; 105879 MW; 5F893B9DF746F731 CRC64;
 Query Match 82.4%; Score 239; DB 1; Length 953;
 Best Local Similarity 76.0%; Pred. No. 9.4e-20;
 Matches 38; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
 |:||||| |: |||||||:|||||:|||||:||| :||| | :|||
 Db 256 SSWTEWSACNVRCGRGWQKRSRTCTNPAPLNGGAFCEGMSVQKITCTSLC 305

RESULT 9

UN5B_MOUSE

ID UN5B_MOUSE STANDARD; PRT; 945 AA.
 AC Q8K1S3; Q6PFH0; Q80Y85; Q9D398;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).
 GN Name=Unc5b; Synonyms=Unc5h2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
 RA Engelkamp D.;
 RT "Cloning of three mouse unc-5 genes and their expression patterns at
 RT mid-gestation.";
 RL Mech. Dev. 118:191-197(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilmung L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.;"
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.;"
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP TISSUE SPECIFICITY.
RX PubMed=12799072;
RA Dalvin S., Anselmo M.A., Prodhan P., Komatsuzaki K., Schnitzer J.J.,
RA Kinane T.B.;
RT "Expression of Netrin-1 and its two receptors DCC and UNC5H2 in the
RT developing mouse lung.;"
RL Gene Expr. Patterns 3:279-283(2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand (By
CC similarity).
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
CC with GNAI2 via its cytoplasmic part (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;
CC IsoId=Q8K1S3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8K1S3-2; Sequence=VSP_011699;
CC !- TISSUE SPECIFICITY: Highly expressed in brain. Expressed in lung
CC during late development. Expressed during early blood vessel
CC formation, in the semicircular canal and in a dorsal to ventral
CC gradient in the retina.
CC !- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity).
CC !- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis (By similarity).
CC !- SIMILARITY: Belongs to the UNC-5 family.
CC !- SIMILARITY: Contains 1 death domain.
CC !- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC !- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC !- SIMILARITY: Contains 2 TSP type-1 domains.
CC !- SIMILARITY: Contains 1 ZU5 domain.
CC

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DR EMBL; AJ487853; CAD32251.1; -.
DR EMBL; AK018177; BAB31108.1; -.
DR EMBL; BC048162; AAH48162.1; ALT_INIT.
DR EMBL; BC057560; AAH57560.1; -.
DR HSSP; P07996; 1LSL.
DR MGD; MGI:894703; Unc5b.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Alternative splicing; Apoptosis; Developmental protein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
KW Transmembrane.

FT	SIGNAL	1	26	Potential.
FT	CHAIN	27	945	Netrin receptor UNC5B.
FT	DOMAIN	27	377	Extracellular (Potential).
FT	TRANSMEM	378	398	Potential.
FT	DOMAIN	399	945	Cytoplasmic (Potential).
FT	DOMAIN	48	145	Ig-like.
FT	DOMAIN	153	242	Ig-like C2-type.
FT	DOMAIN	246	300	TSP type-1 1.
FT	DOMAIN	302	354	TSP type-1 2.
FT	DOMAIN	541	644	ZU5.
FT	DOMAIN	865	943	Death.
FT	SITE	412	413	Cleavage (by caspase-3) (By similarity).
FT	SITE	707	725	Interaction with DCC (By similarity).
FT	DISULFID	69	128	By similarity.
FT	DISULFID	174	225	By similarity.
FT	CARBOHYD	222	222	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	347	347	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	356	367	NQRTLNDPKSHP -> T (in isoform 2). /FTId=VSP_011699.
FT	CONFLICT	238	238	T -> A (in Ref. 2).
FT	CONFLICT	394	394	V -> E (in Ref. 2).
FT	CONFLICT	679	679	T -> S (in Ref. 2).
FT	CONFLICT	874	874	N -> D (in Ref. 2).
SO	SEQUENCE	945	AA; 103738 MW;	80E896F0F0E06012 CRC64;

Query Match 82.1%; Score 238; DB 1; Length 945;
 Best Local Similarity 78.0%; Pred. No. 1.2e-19;
 Matches 39; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTCNPAPLNGGAFCEGQNVQKTACATLC 50
|:| ||| ||| ||| ||| ||| :|:| ||| ||| ||| ||| ||| ||| :|:
Db 250 SSWAEWSPCSNRGGRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTTVC 299

RESULT 10
UN5B_RAT
ID UN5B_RAT STANDARD; PRT; 945 AA.
AC 008722;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).
GN Name=Unc5b; Synonyms=Unc5h2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RX MEDLINE=97271897; PubMed=9126742;
RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
RA Tessier-Lavigne M.;
RT "Vertebrate homologues of *C. elegans* UNC-5 are candidate netrin
RT receptors.";
RL Nature 386:833-838(1997).
RN [2]

RP FUNCTION, AND INTERACTION WITH DCC.
RX PubMed=10399920;
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
RA Stein E.;
RT "A ligand-gated association between cytoplasmic domains of UNC5 and
RT DCC family receptors converts netrin-induced growth cone attraction to
RT repulsion.";
RL Cell 97:927-941(1999).
RN [3]
RP FUNCTION, AND MUTAGENESIS OF ASP-412.
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
RL EMBO J. 20:2715-2722(2001).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand.
CC -!- SUBUNIT: Interacts with GNAI2 via its cytoplasmic part (By
CC similarity). Interacts with the cytoplasmic part of DCC.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
CC neurons. Expressed in the developing sensory ganglia that flank
CC the spinal cord from E12, peaking at E14. Expressed in the roof
CC plate region of the spinal cord from E14.
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U87306; AAB57679.1; -.
DR HSSP; P07996; 1LSL.
DR RGD; 621756; Unc5h2.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.

DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 945 Netrin receptor UNC5B.
 FT DOMAIN 27 377 Extracellular (Potential).
 FT TRANSMEM 378 398 Potential.
 FT DOMAIN 399 945 Cytoplasmic (Potential).
 FT DOMAIN 48 145 Ig-like.
 FT DOMAIN 153 242 Ig-like C2-type.
 FT DOMAIN 246 300 TSP type-1 1.
 FT DOMAIN 302 354 TSP type-1 2.
 FT DOMAIN 541 644 ZU5.
 FT DOMAIN 865 943 Death.
 FT SITE 412 413 Cleavage (by caspase-3).
 FT SITE 707 725 Interaction with DCC.
 FT DISULFID 69 128 By similarity.
 FT DISULFID 174 225 By similarity.
 FT CARBOHYD 222 222 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc. . .) (Potential).
 FT MUTAGEN 412 412 D->N: Abolishes cleavage by caspase-3 and
 subsequent induction of apoptosis.
 SO SEQUENCE 945 AA: 103520 MW: 6E9C2A262E560B9B CRC64:

```

Query Match           82.1%;  Score 238;  DB 1;  Length 945;
Best Local Similarity 78.0%;  Pred. No. 1.2e-19;
Matches 39;  Conservative 4;  Mismatches 7;  Indels 0;  Gaps 0;

Qy      1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
       ||:|| ||| || |||||||||:||:||||||||||| ||||| :|||
Db      250 SSWAEGSPCSNRGGRGWQKRTCTNPAPLNGGAFCEGQACQKTACTTVC 299

```

RESULT 11

UN5D MOUSE

ID UN5D_MOUSE STANDARD; PRT; 956 AA.
AC Q8K1S2;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4).
GN Name=Unc5d; Synonyms=Unc5h4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFIICTY.
RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
RA Engelkamp D.;
RT "Cloning of three mouse Unc5 genes and their expression patterns at
RT mid-gestation.";
RL Mech. Dev. 118:191-197(2002).
CC -!- FUNCTION: Receptor for netrin involved in cell migration. May be
CC involved in axon guidance by mediating axon repulsion of neuronal
CC growth cones in the developing nervous system upon ligand binding.
CC Axon repulsion in growth cones may be caused by its association
CC with DCC that may trigger signaling for repulsion. It also acts as
CC a dependence receptor required for apoptosis induction when not
CC associated with netrin ligand (By similarity).
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in developing limb and mammary
CC gland.
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis (By similarity).
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----
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CC -----
DR EMBL; AJ487854; CAD32252.1; -.
DR HSSP; P07996; 1LSL.
DR MGD; MGI:2389364; Unc5d.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PRO1705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.

DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 30 Potential.
 FT CHAIN 31 956 Netrin receptor UNC5D.
 FT DOMAIN 31 382 Extracellular (Potential).
 FT TRANSMEM 383 403 Potential.
 FT DOMAIN 404 956 Cytoplasmic (Potential).
 FT DOMAIN 52 149 Ig-like.
 FT DOMAIN 151 242 Ig-like C2-type.
 FT DOMAIN 250 304 TSP type-1 1.
 FT DOMAIN 306 358 TSP type-1 2.
 FT DOMAIN 543 645 ZU5.
 FT DOMAIN 862 939 Death.
 FT SITE 419 420 Cleavage (by caspase-3) (By similarity).
 FT SITE 706 724 Interaction with DCC (By similarity).
 FT DISULFID 73 132 By similarity.
 FT DISULFID 178 229 By similarity.
 FT CARBOHYD 115 115 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 226 226 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 351 351 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 379 379 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 956 AA; 106351 MW; DFDF07839C10C68D CRC64;

Query Match 82.1%; Score 238; DB 1; Length 956;
 Best Local Similarity 76.0%; Pred. No. 1.2e-19;
 Matches 38; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSTNPAPLNGGAFCEGQNVQKTACATLC 50
 |:||||| : |||||||:|||||||:||||| :||| |||
 Db 254 SSWTEWSACNVRCGRGWQKRSRTCTNPAPLNGGAFCEGMSVQKITCTALC 303

RESULT 12

UN5B_XENLA

ID UN5B_XENLA STANDARD; PRT; 943 AA.
 AC Q8JGT4;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (UNC-5 homolog) (Protein XUNC-5).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=22239703; PubMed=12351179; DOI=10.1016/S0925-4773(02)00215-0;
 RA Anderson R.B., Holt C.E.;
 RT "Expression of UNC-5 in the developing Xenopus visual system.";
 RL Mech. Dev. 118:157-160(2002).
 CC --!- FUNCTION: Receptor for netrin required for axon guidance. Mediates

CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: In the developing visual system, it is
 CC expressed within the developing optic vesicles and later become
 CC restricted to the dorsal ciliary marginal zone, a site of
 CC retinoblast proliferation and differentiation.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AY099459; AAM34486.1; -.
 DR HSSP; P07996; 1LSI.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PRO1705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Developmental protein; Immunoglobulin domain; Phosphorylation;
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 30 Potential.
 FT CHAIN 31 943 Netrin receptor UNC5B.
 FT DOMAIN 31 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 943 Cytoplasmic (Potential).
 FT DOMAIN 51 148 Ig-like.
 FT DOMAIN 150 245 Ig-like C2-type.
 FT DOMAIN 249 303 TSP type-1 1.
 FT DOMAIN 305 357 TSP type-1 2.
 FT DOMAIN 540 643 ZU5.

FT DOMAIN 863 941 Death.
FT DISULFID 72 131 By similarity.
FT DISULFID 177 228 By similarity.
FT CARBOHYD 225 225 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 350 350 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 943 AA; 105083 MW; A024E24A7EDB6175 CRC64;

Query Match 75.5%; Score 219; DB 1; Length 943;
Best Local Similarity 70.0%; Pred. No. 2.2e-17;
Matches 35; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 STWTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTACATLC 50
|:||||| |: || |||||:|:||||||| |||| || || |:|
Db 253 SSWTEWSPCNNRCGHGWQKRTRTCTNPAPLNGGTMCEGQQYQKFACNTMC 302

RESULT 13

Q8BVQ2

ID Q8BVQ2 PRELIMINARY; PRT; 335 AA.
AC Q8BVQ2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4932412F09 product:sema domain, seven thrombospondin
DE repeats (type 1 and type 1-like), transmembrane domain (TM) and short
DE cytoplasmic domain, (semaphorin) 5A, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AK077021; BAC36572.1; -.

DR HSSP; P07996; 1LSL.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR008085; TSP_1.

DR Pfam; PF00090; TSP_1; 4.

DR PRINTS; PR01705; TSP1REPEAT.

DR SMART; SM00209; TSP1; 4.

DR PROSITE; PS50092; TSP1; 4.

KW Transmembrane.

SQ SEQUENCE 335 AA; 37185 MW; A6A451219EFC530D CRC64;

Query Match 51.0%; Score 148; DB 2; Length 335;

Best Local Similarity 54.5%; Pred. No. 2.1e-09;

Matches 24; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
|| || || :|| |:| | |||:|| | :|| | ||| :|

Db 92 WTSWSPCSTTCIGFQVRQRCSNPTPRHGGRVCVGQNREERYC 135

RESULT 14

Q8BXU8

ID Q8BXU8 PRELIMINARY; PRT; 844 AA.
AC Q8BXU8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:A730090007 product:sema domain, seven
DE thrombospondin repeats (type 1 and type 1-like), transmembrane domain
DE (TM) and short cytoplasmic domain, (semaphorin) 5A, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK043386; BAC31531.1; -.
 DR HSSP; P07996; 1LSL.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR Pfam; PF00090; TSP_1; 4.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR SMART; SM00209; TSP1; 4.
 DR PROSITE; PS50092; TSP1; 4.
 KW Transmembrane.
 SQ SEQUENCE 844 AA; 94673 MW; 19D4D8DAB36FBEA5 CRC64;

Query Match 51.0%; Score 148; DB 2; Length 844;
 Best Local Similarity 54.5%; Pred. No. 5e-09;
 Matches 24; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
 Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
 || || || :|| |:| | |||:|| | :|| | ||| :|
 Db 601 WTSWSPCSTTCGIGFQVRQRSCSNPTPRHGGRVCVGQNREERYC 644

RESULT 15
 SM5A_HUMAN
 ID SM5A_HUMAN STANDARD; PRT; 1074 AA.
 AC Q13591; O60408;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Semaphorin 5A precursor (Semaphorin F) (Sema F).
 GN Name=SEMA5A; Synonyms=SEMAF;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98125554; PubMed=9464278; DOI=10.1006/bbrc.1997.8027;
RA Simmons A.D., Puschel A.W., McPherson J.D., Overhauser J., Lovett M.;
RT "Molecular cloning and mapping of human semaphorin F from the Cri-du-
RT chat candidate interval.";
RL Biochem. Biophys. Res. Commun. 242:685-691(1998).
RN [2]
RP SEQUENCE OF 1-494 FROM N.A.
RA Kalicki J., Harmon G.;
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP INTERACTION WITH PLXNB3.
RX PubMed=15218527; DOI=10.1038/sj.embor.7400189;
RA Artigiani S., Conrotto P., Fazzari P., Gilestro G.F., Barberis D.,
RA Giordano S., Comoglio P.M., Tamagnone L.;
RT "Plexin-B3 is a functional receptor for semaphorin 5A.";
RL EMBO Rep. 5:710-714(2004).
CC -!-- FUNCTION: May act as positive axonal guidance cues.
CC -!-- SUBUNIT: Binds PLXNB3.
CC -!-- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!-- SIMILARITY: Belongs to the semaphorin family.
CC -!-- SIMILARITY: Contains 1 Sema domain.
CC -!-- SIMILARITY: Contains 7 TSP type-1 domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U52840; AAC09473.1; -.
DR EMBL; AC004615; AAC14668.1; -.
DR PIR; JC5928; JC5928.
DR HSSP; P07996; 1LSL.
DR Genew; HGNC:10736; SEMA5A.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP_1; 6.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 6.
DR PROSITE; PS51004; SEMA; 1.

DR PROSITE; PS50092; TSP1; 6.
 KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 1074 Semaphorin 5A.
 FT DOMAIN 23 968 Extracellular (Potential).
 FT TRANSMEM 969 989 Potential.
 FT DOMAIN 990 1074 Cytoplasmic (Potential).
 FT DOMAIN 35 484 Sema.
 FT DOMAIN 540 593 TSP type-1 1.
 FT DOMAIN 595 651 TSP type-1 2.
 FT DOMAIN 653 702 TSP type-1 3.
 FT DOMAIN 707 765 TSP type-1 4.
 FT DOMAIN 784 839 TSP type-1 5.
 FT DOMAIN 841 896 TSP type-1 6.
 FT DOMAIN 897 944 TSP type-1 7.
 FT DISULFID 104 114 By similarity.
 FT DISULFID 131 140 By similarity.
 FT DISULFID 278 320 By similarity.
 FT DISULFID 487 504 By similarity.
 FT DISULFID 496 513 By similarity.
 FT CARBOHYD 142 142 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 168 168 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 227 227 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 277 277 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 323 323 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 367 367 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 437 437 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 591 591 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 717 717 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 933 933 N-linked (GlcNAc. . .) (Potential).
 FT CONFLICT 56 56 A -> V (in Ref. 2).
 FT CONFLICT 149 149 A -> T (in Ref. 2).
 FT CONFLICT 382 382 V -> M (in Ref. 2).
 FT CONFLICT 494 494 S -> R (in Ref. 2).
 SQ SEQUENCE 1074 AA; 120570 MW; EE3DB763CBE29407 CRC64;

Query Match 51.0%; Score 148; DB 1; Length 1074;
 Best Local Similarity 54.5%; Pred. No. 6.2e-09;
 Matches 24; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 3 WTEWSVCSASCGRGWQKRSRSCTNPAPLNGGAFCEGQNVQKTAC 46
 || || || :|| |:| | |||:|| | :|| | ||| :: |
 Db 601 WTSWSPCSTTCGIGFQVRQRSCSNPTPRHGGRVCVGQNREERYC 644

Search completed: March 1, 2005, 09:03:37
 Job time : 11.1466 secs